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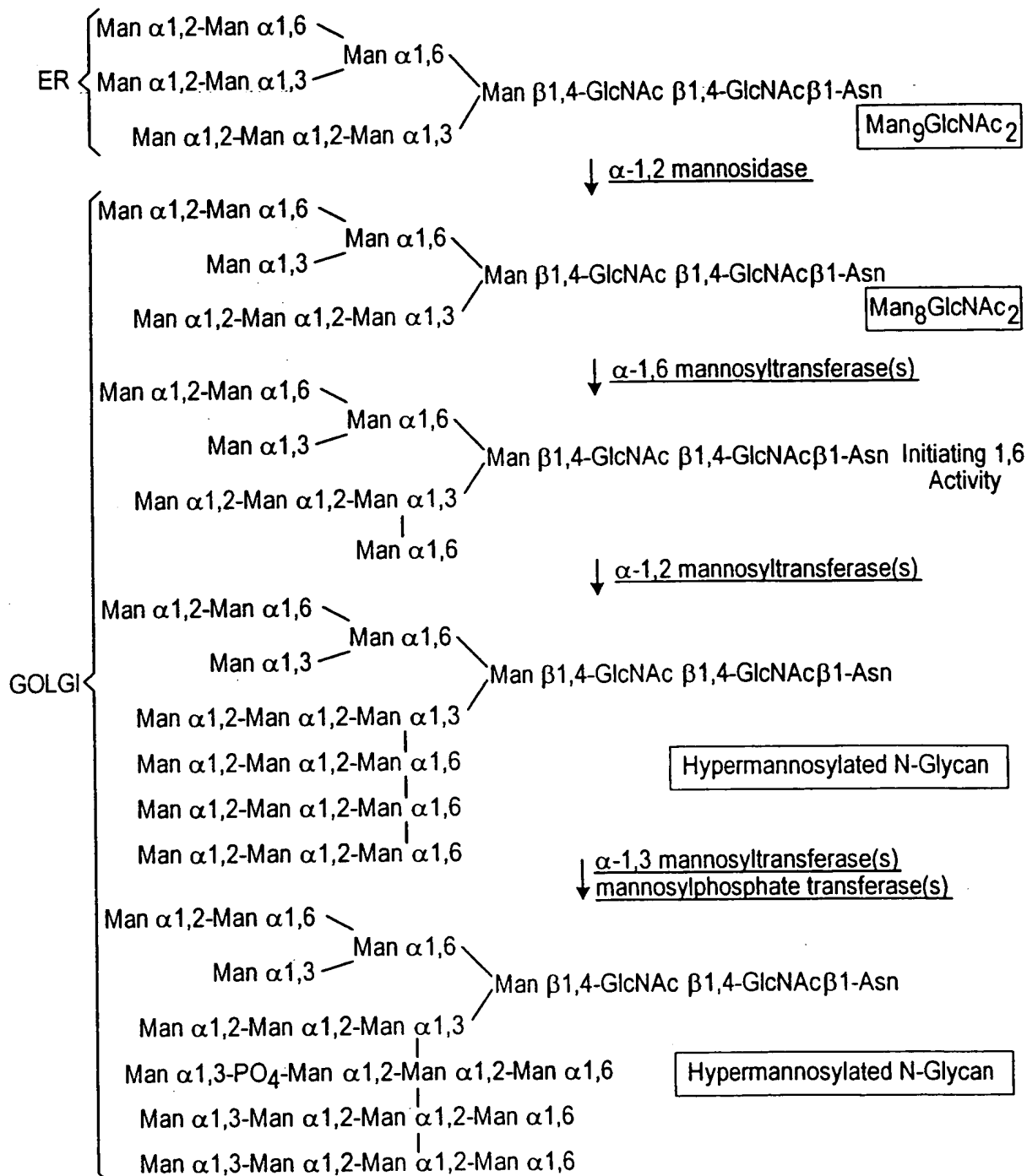


FIG. 1A

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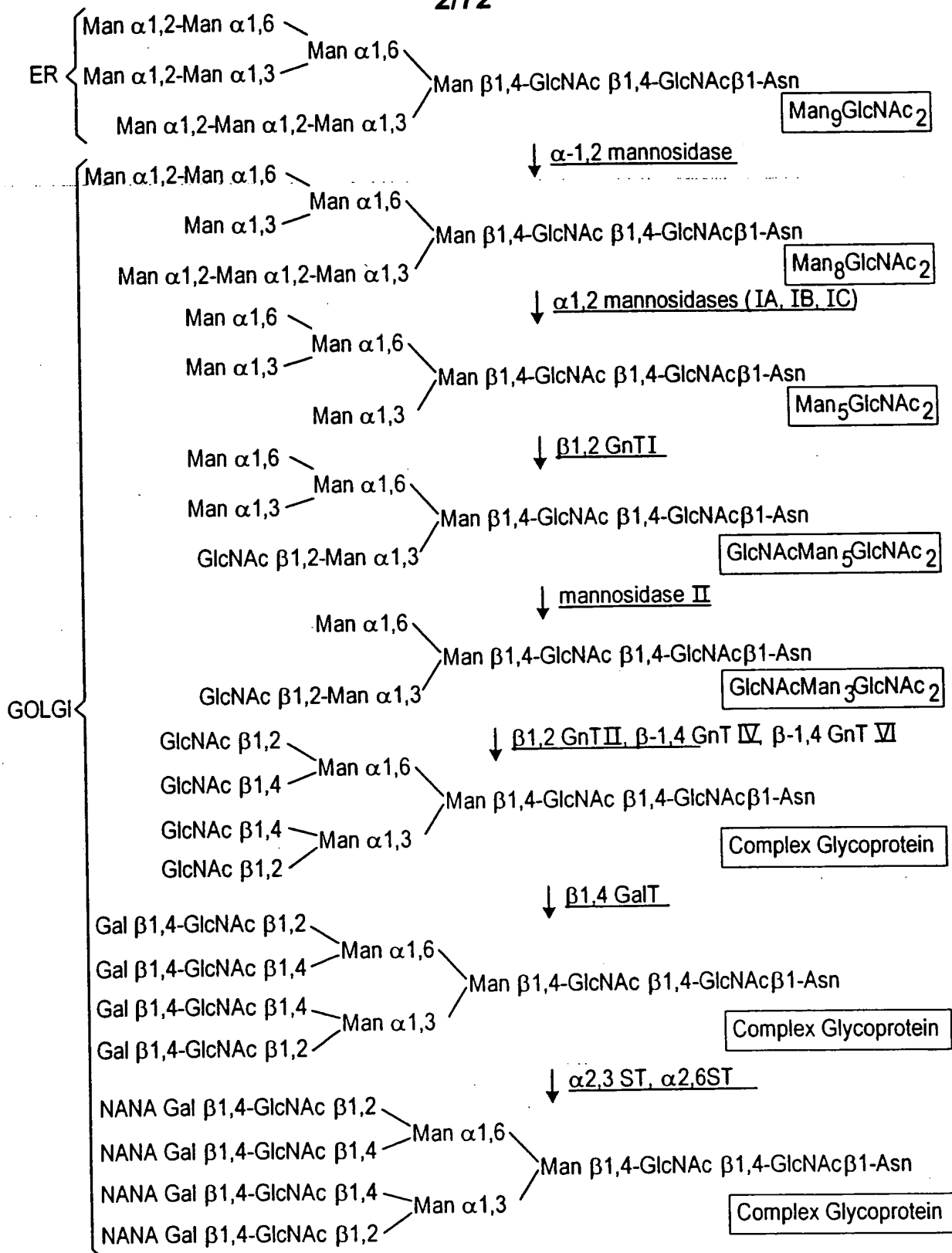


FIG. 1B

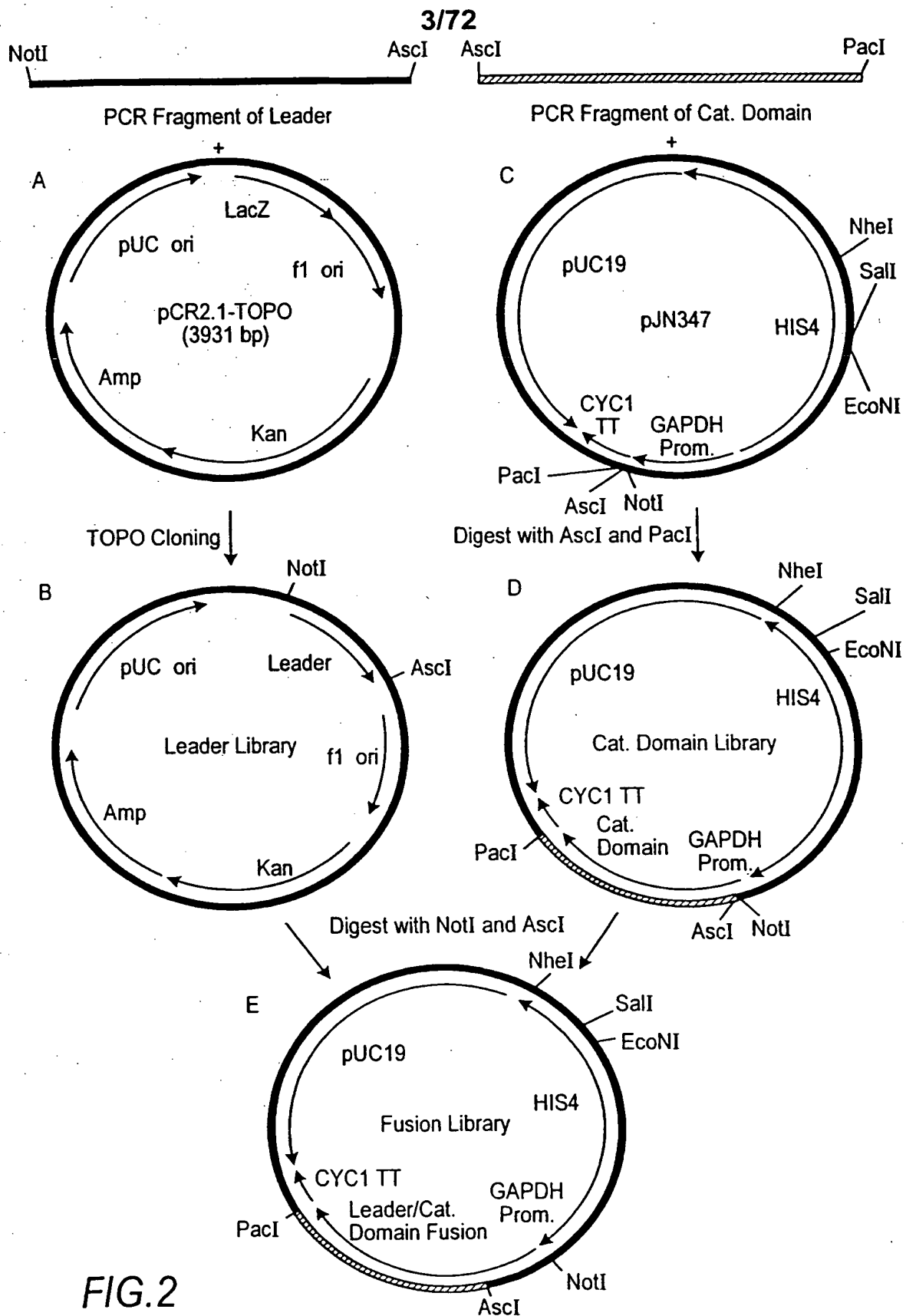


FIG.2

M. musculus alpha-1,2-mannosidase IA open reading frame. The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.

```

1  atgccgtggggcctgttgccgctcttcagtagccctggggcgggcgccctgggcagtgccctggggggggttgccggcgaggagggg
1▶ M P V G G L L P L F S S P G G G L G S G L G G L G G L G G R K G
97  tctggcccgctgccttcgcctcaccgagaagtctgtgtgtgttcagcgcccttcacgcgtotgttcgggggcaatc
33▶ S G P A A F R L T E K F V L L L V F S A F I T L C F G A I
184  ttcttctgctgactcctccaaagctcagcggtcctgttcactccaaacctgttcagcccgccggcgagcacaagcccggtctcg
62▶ F F L P D S S K L L S G V L F H S N P A L Q P P A E H K P G L
      d65 primer
278  gggcgctgaggatgcccgccgaggaggagagtcgcgcaccgcagggaagcgccgctggggaccctggagctggactggaagacaacttagcca
93▶ G A R A E D A A E G R V R H R E E G A P G D P G A G L E D N L A
      d105 primer
374  ggatccgcgaaaccacgagcggtctctcagggaagccaaaggagaccctgcagaagctgccggaggagatccaaagagacattctgctggagaagg
125▶ R I R E N H E R A L R E A K E T L Q K L P E E I Q R D I L L E K
470  aaaagggtggccaggaccagctgcgtgacaaaggatctgttaggggcttgcccaaggtggacttctgcccccggtcggttagagaacgggagc
157▶ E K V A Q D Q L R D K D L F R G L P K V D F L P P V G V E N R E
      d187 primer
566  ccgtgacgccaccatccgtgagaagagggcaagatcaaaagagatgaccccatgcttggaataattataacgctatgcgtggggc
189▶ P A D A T I R E K R A K I K E M M T H A W N N Y K R Y A W G

```

FIG. 3

655 ttgaacgaactgaacacctatatacaaaagaaggccattcaagcagtttgtttggcaacatcaaaaggagctacaatagtagatg
 219▶ L N E L K P I S K E G H S S L F G N I K G A T I V D
 737 cctggatacccttttcattatgggcataagactgaatttcaagaagctaaatcggtgattaaaaatatttagatttttaa
 246▶ A L D T L F I M G M K T E F Q E A K S W I K K Y L D F N
 819 tgtgaatgctgaagtttctgttttgaagtcaacatacgccttcgctggtggaactgtgtcagcctactatttgcgggagag
 273▶ V N A E V S V F E V N I R F V G G L L S A Y Y L S G E
 901 gagatatctgaaagaagcagtggaacttggggtaaaattgctacctgcattcactccctcttgaataccttgggcat
 301▶ E I F R K K A V E L G V K L L P A F H T P S G I P W A
 983 tgcgaatatgaaaagtgggacggtgggaactggccctggccctctggaggcagcagtagtccctggccgaatttggaaactct
 328▶ L L N M K S G I G R N W P W A S G S S I L A E F G T L
 1065 gcatttagagtttatgcacttgtccacttatcaggagaccagctcttggccgaaaaggttatgaaaattcgaacagtggtg
 355▶ H L E F M H L S H L S G D P V F A E K V M K I R T V L
 1147 acaaaactggacaaaccagaaggcctttatcctaactatctgaaccccaagtagtggaactgtgggtggtcaacatcatgtgtcgg
 383▶ N K L D K P E G L Y P N Y L N P S S G Q W G Q H H V S
 1229 ttggaggacttggagacagcttttatgaatatgttgaagcgtggttaattgtctgacaagacagatctcgaagccaagaa
 410▶ V G G L G D S F Y E Y L L K A W L M S D K T D L E A K K
 1311 gatgtatttgcgtgttcaggccatcgagactcaactgtgacgcgaactgaagtcgaagtggtgggactaacgtacatcgacagtggtg
 437▶ M Y F D A V Q A I E T H L I R K S S G G L T Y I A E W
 1393 aagggggcctctctgaaacacaagatgggccacctgacgtgcttgcaggaggcagctgttgcacttggggcagatggagctc
 465▶ K G G L L E H K M G H L T C F A G G M F A L G A D G A
 1475 cggaagcccgcccaacactacctgaactcggagctgaattggccgcacttgcacgaattcttataatcgtagatgtg
 492▶ P E A R A Q H Y L E L G A E I A R T C H E S Y N R T Y V
 1557 gaagttgggacgggaagcgtttcgaatttgatggcgtgtggaagctattgccacgaggcgaataatgaaaagtattacaactcta
 519▶ K L G P E A F R F D G G V E A I A T R Q N E K Y Y I L
 1639 cgcccgaggtcatcgagacatacatgtacatgtggcgactgactcacgaaccccaagtaaggacacctgggcccgggaagccg
 547▶ R P E V I E T Y M Y M W R L T H D P K Y R T W A W E A
 1721 tggaggctctagaagtcactgcagagtggaacggaggctactcaggctcagggtggttaccattgcccgtgagaggttatga
 574▶ V E A L E S H C R V N G G Y S G L R D V Y I A R E S Y D
 1803 cgatgtccagcaagtttctcctggcagagacactgaagtattgtacttgatatttccgatgtatgcaccttcttccacta
 601▶ D V Q Q S F F L A E T L K Y L Y L I F S D D L L P L
 1885 gaacactggtcttcaacacccagggtcctccttccctatactccgtgaacagagaaggaattgatggcaagagaatga
 629▶ E H W I F N T E A H P F P I L R E Q K E I D G K E K

FIG. 3 CONT

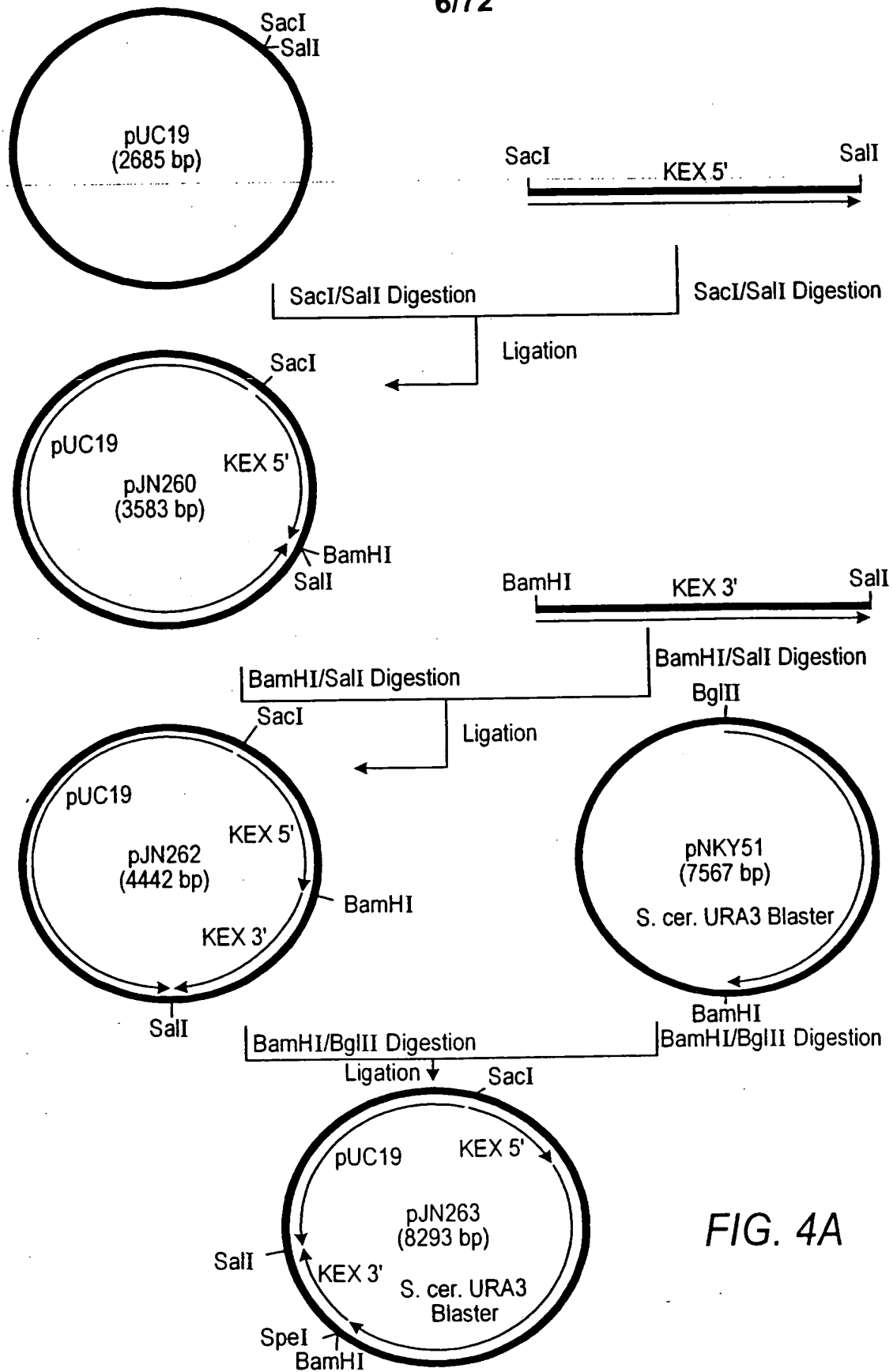


FIG. 4A

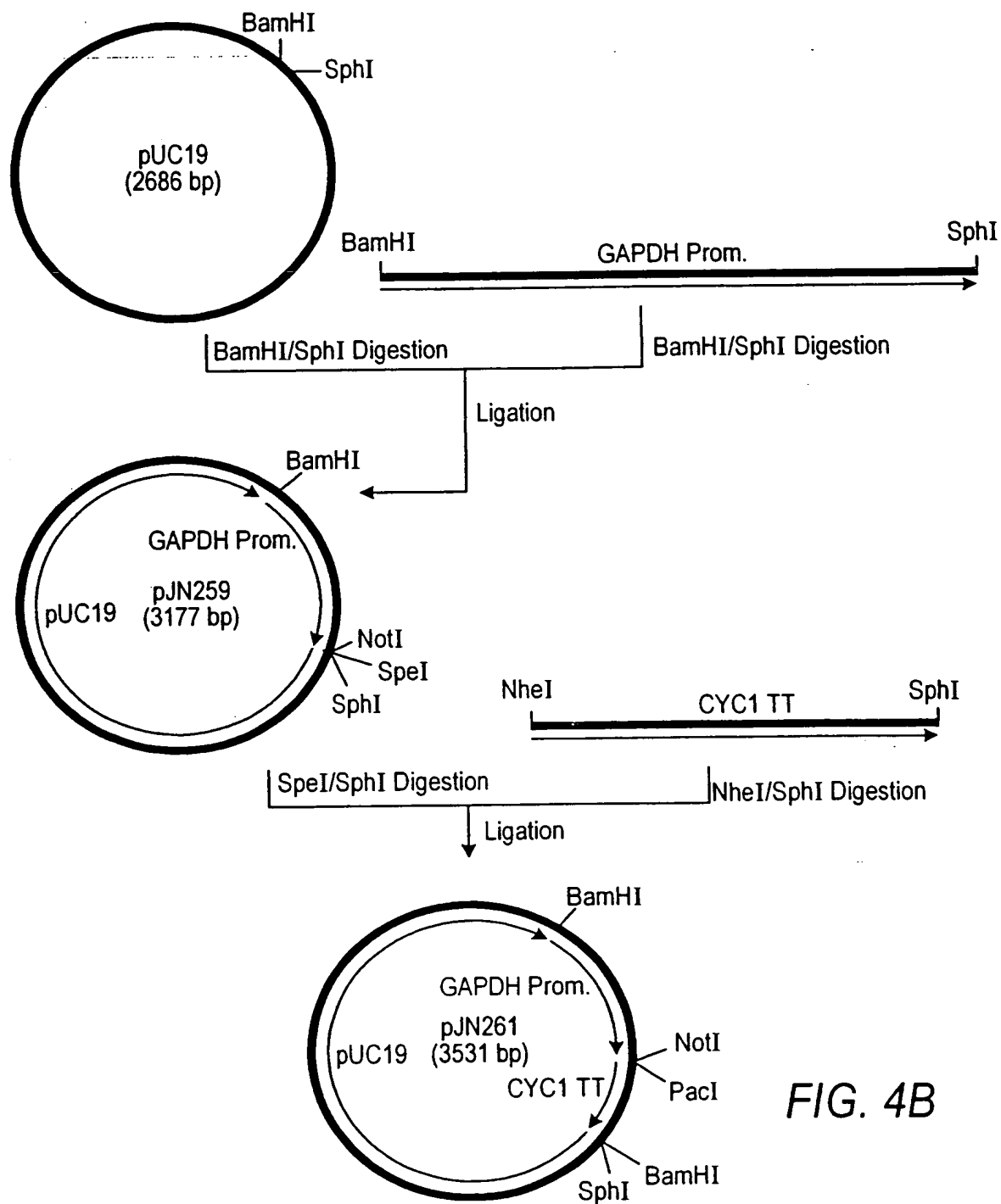


FIG. 4B

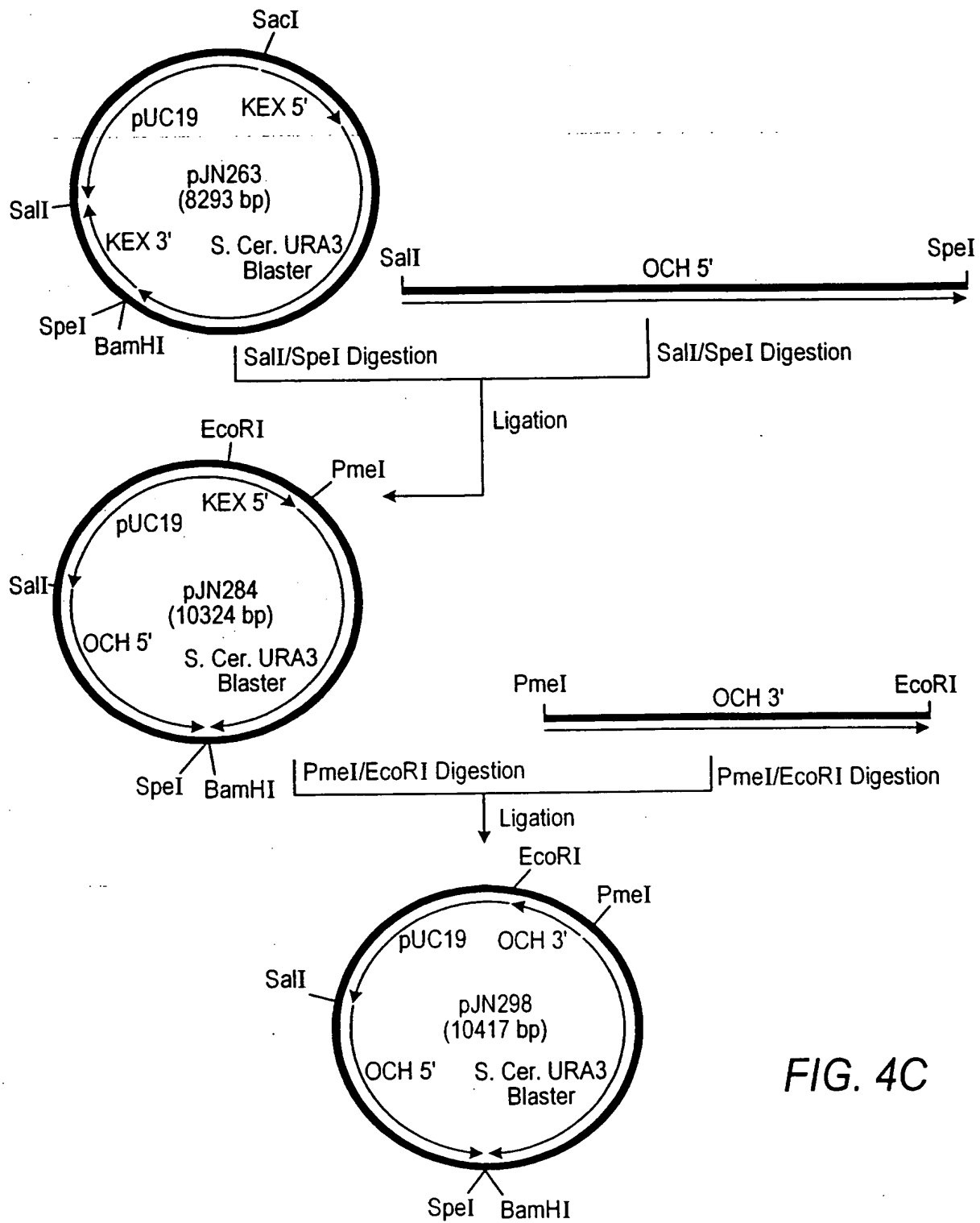


FIG. 4C

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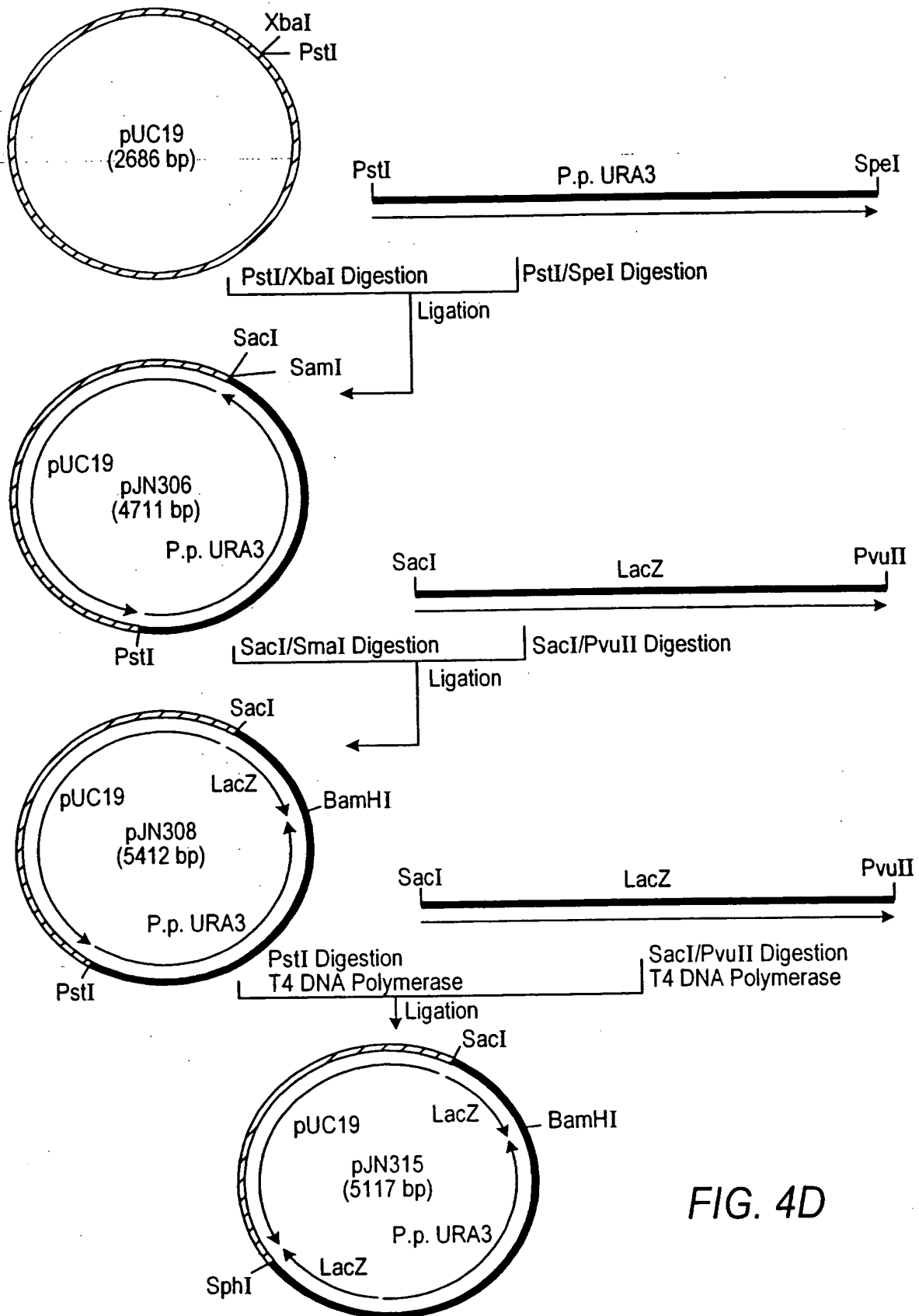


FIG. 4D

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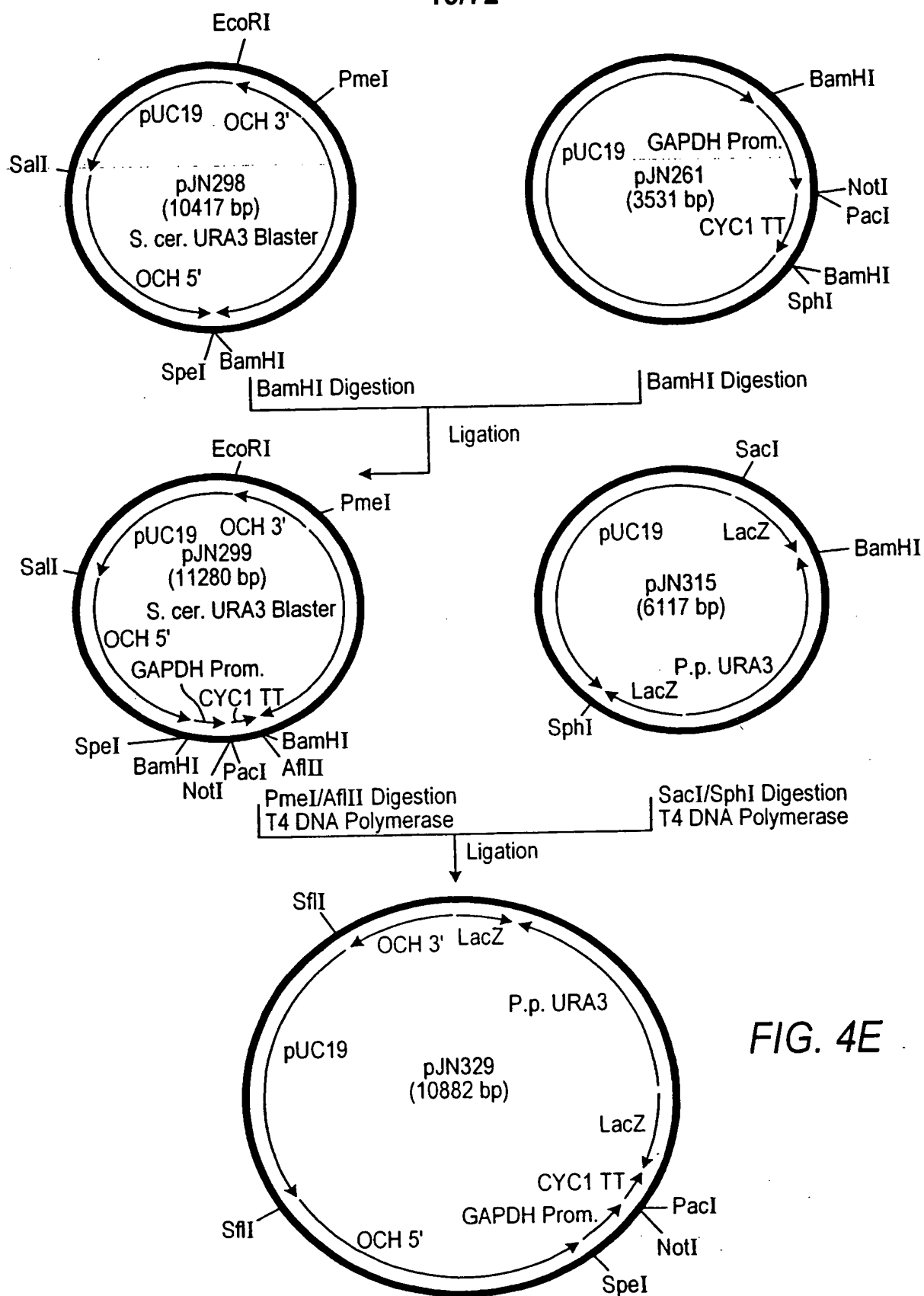


FIG. 4E

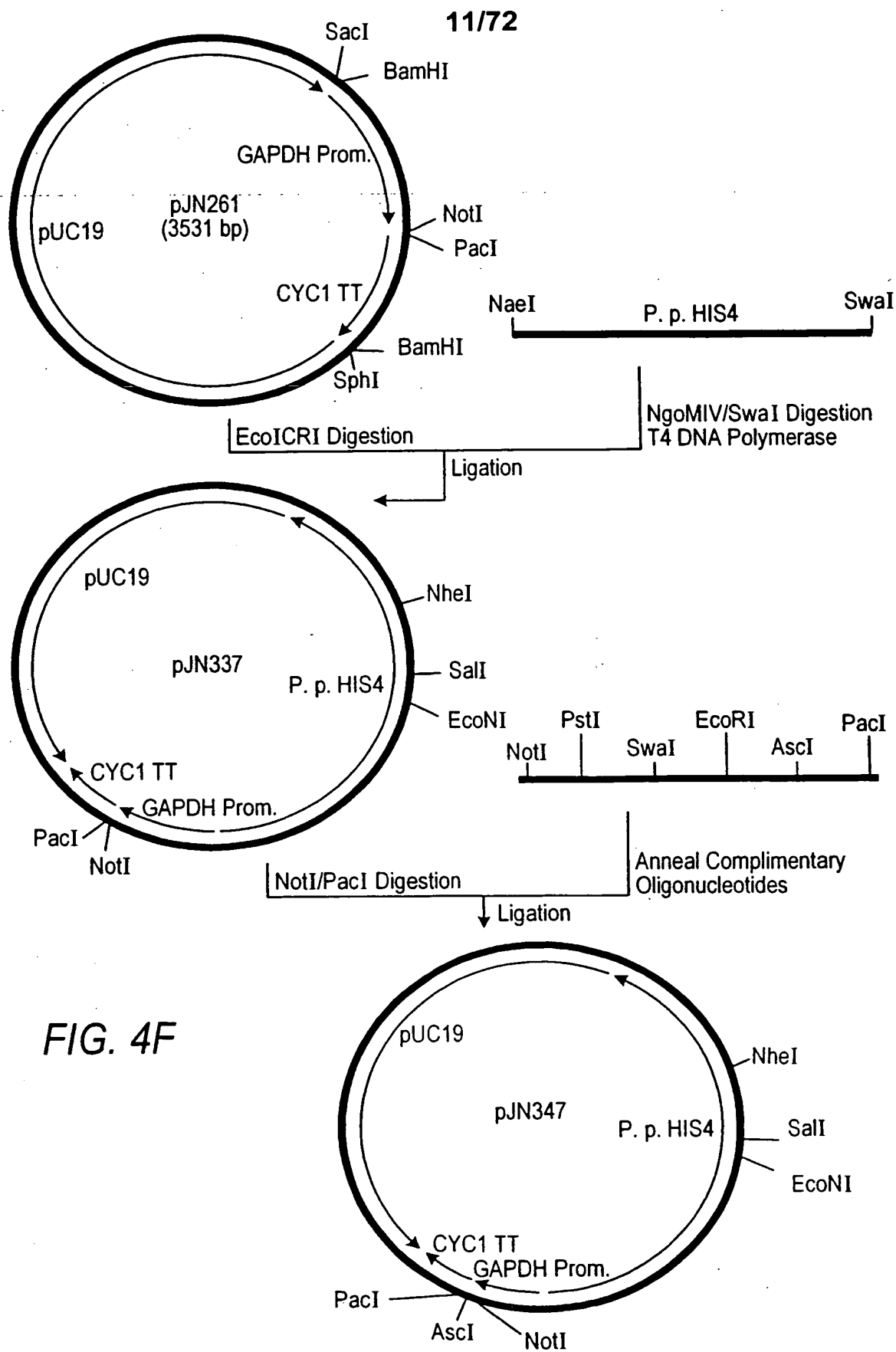
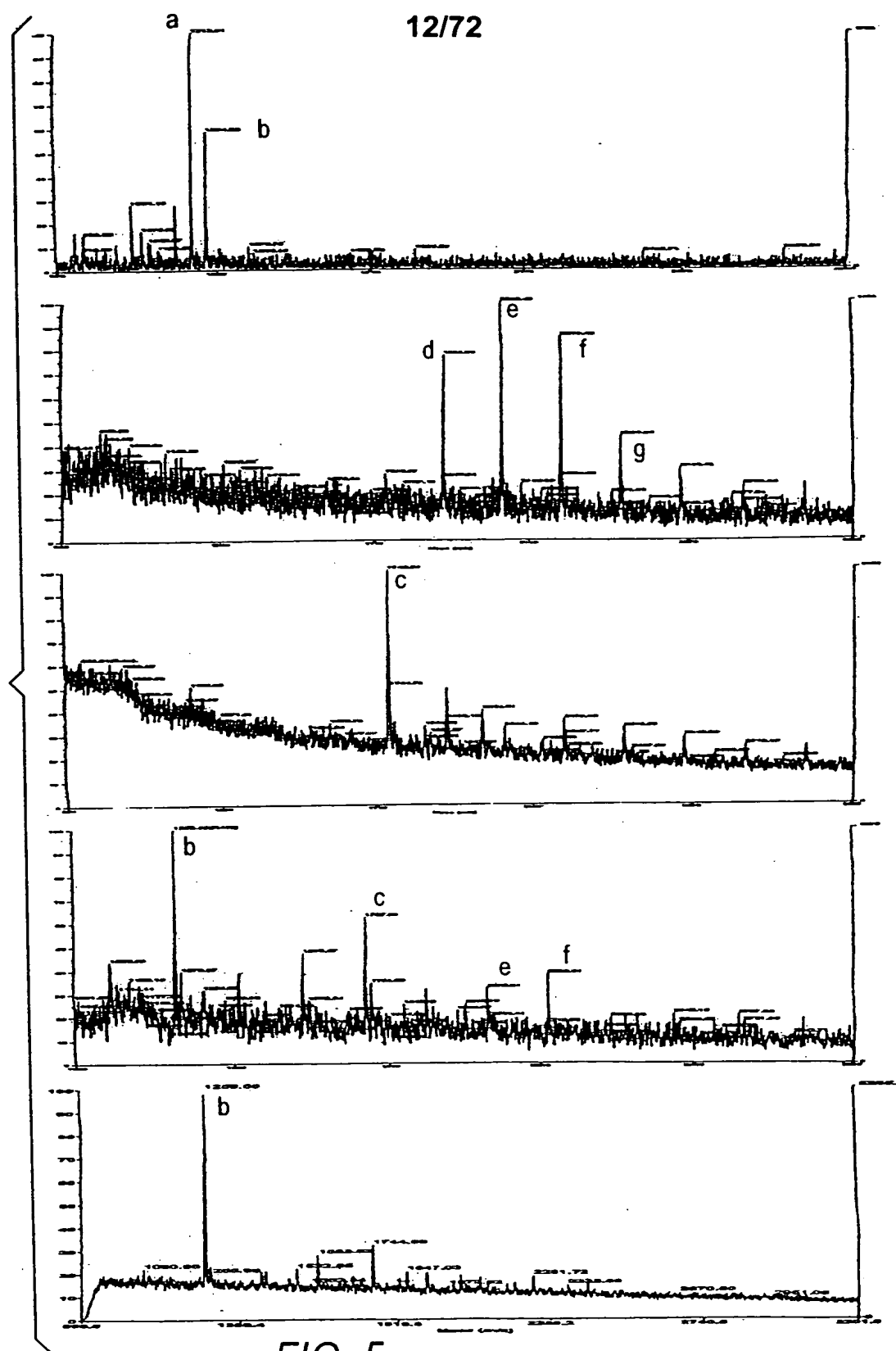


FIG. 4F



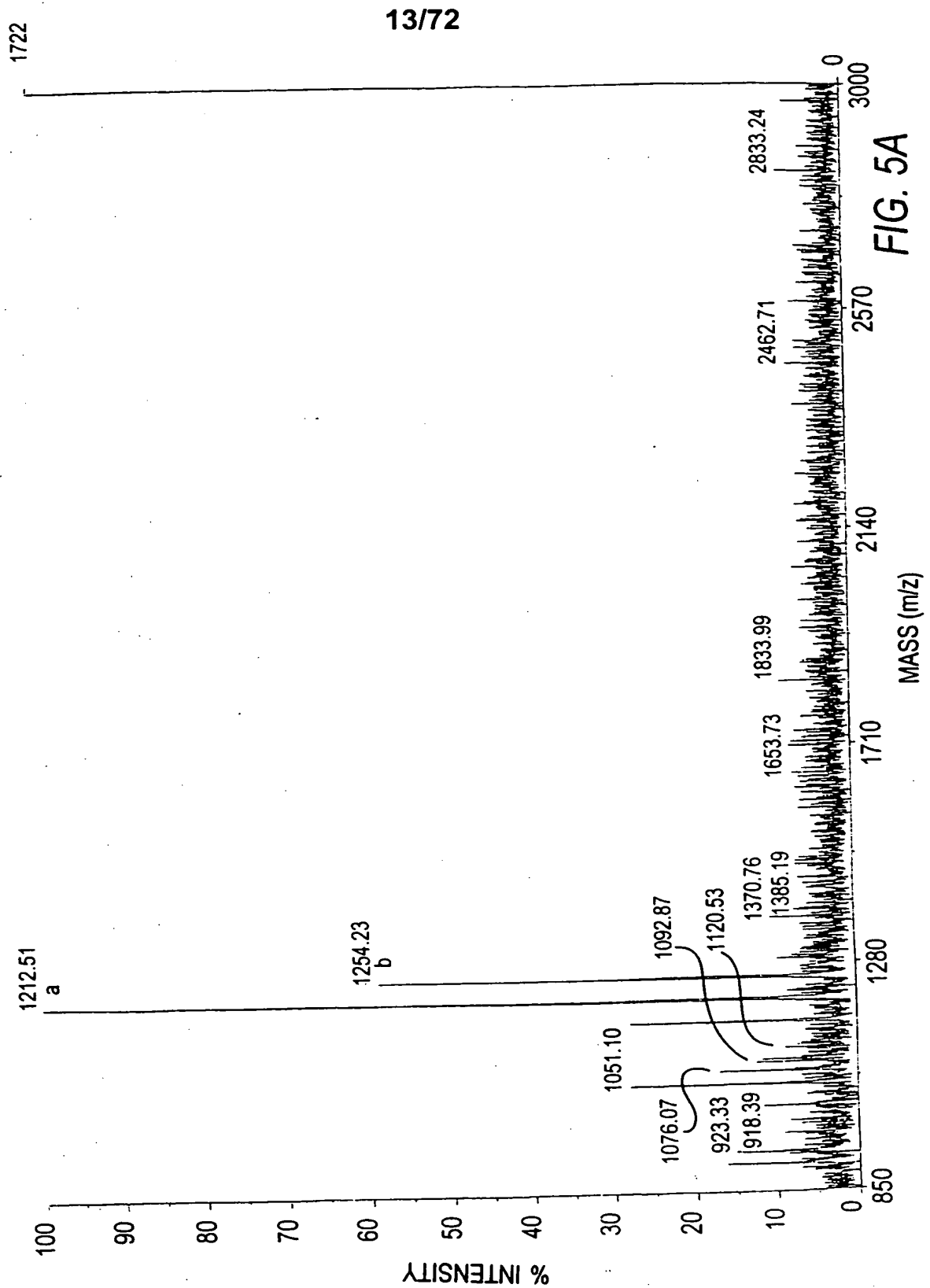


FIG. 5A

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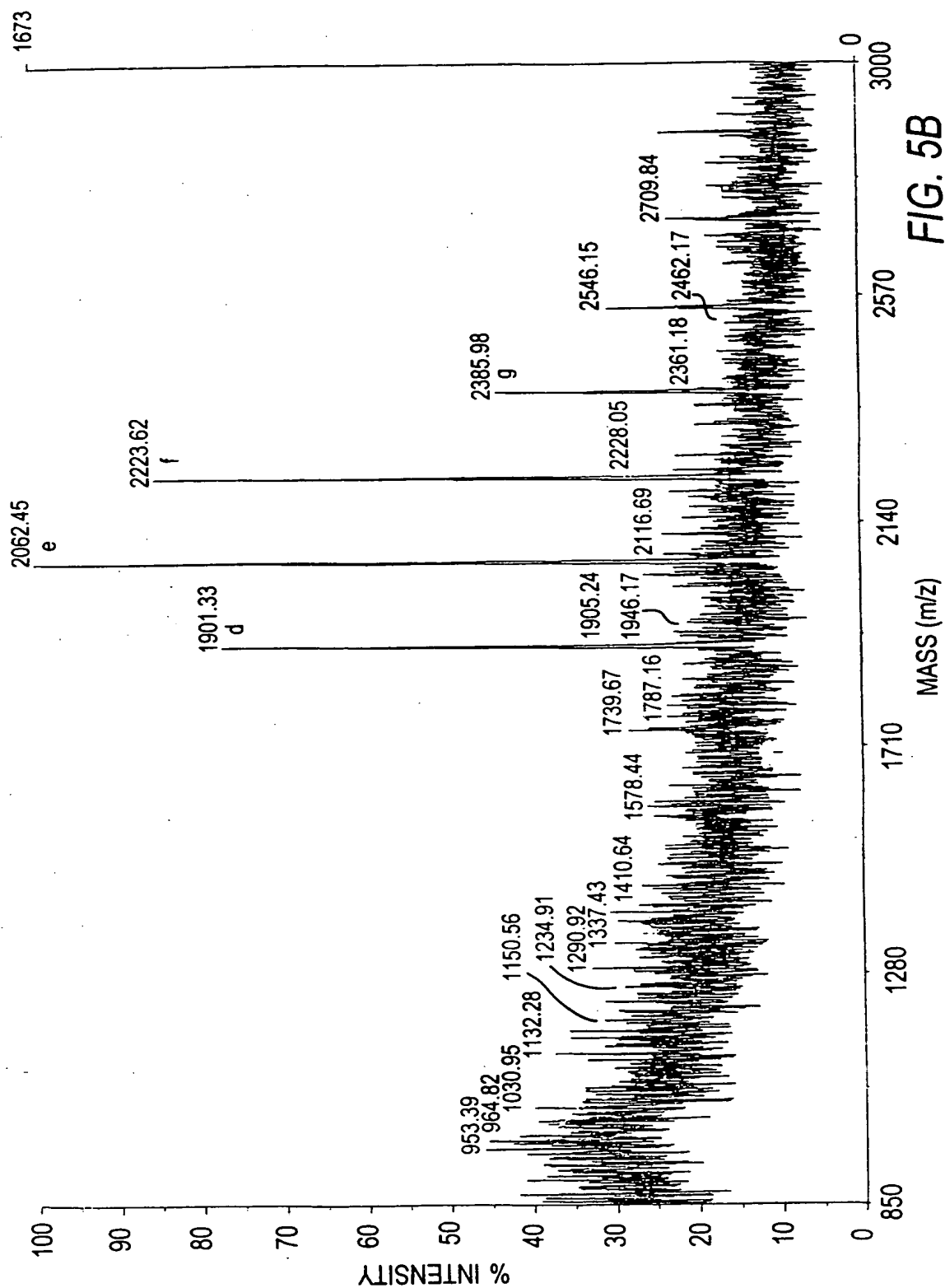


FIG. 5B

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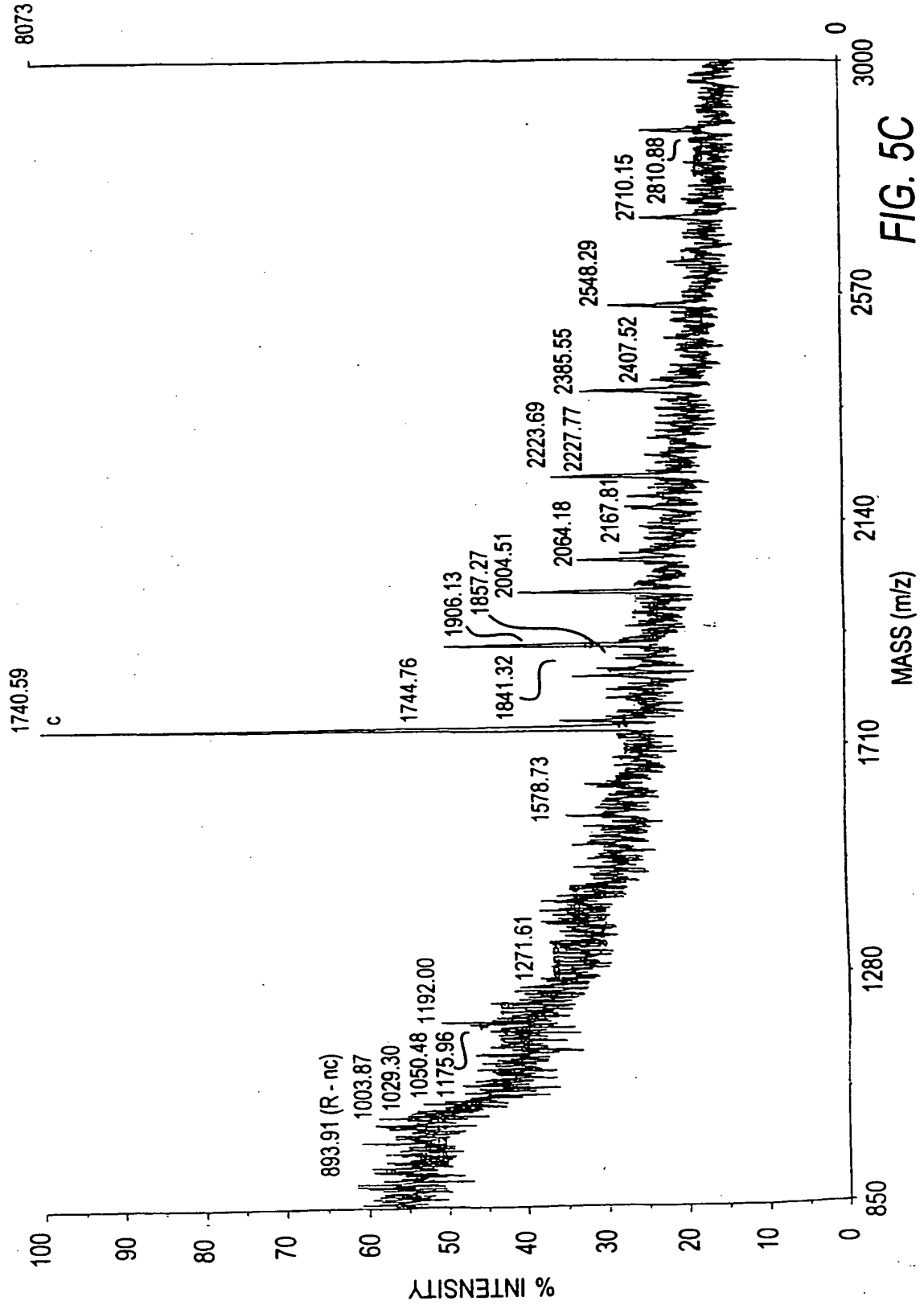


FIG. 5C

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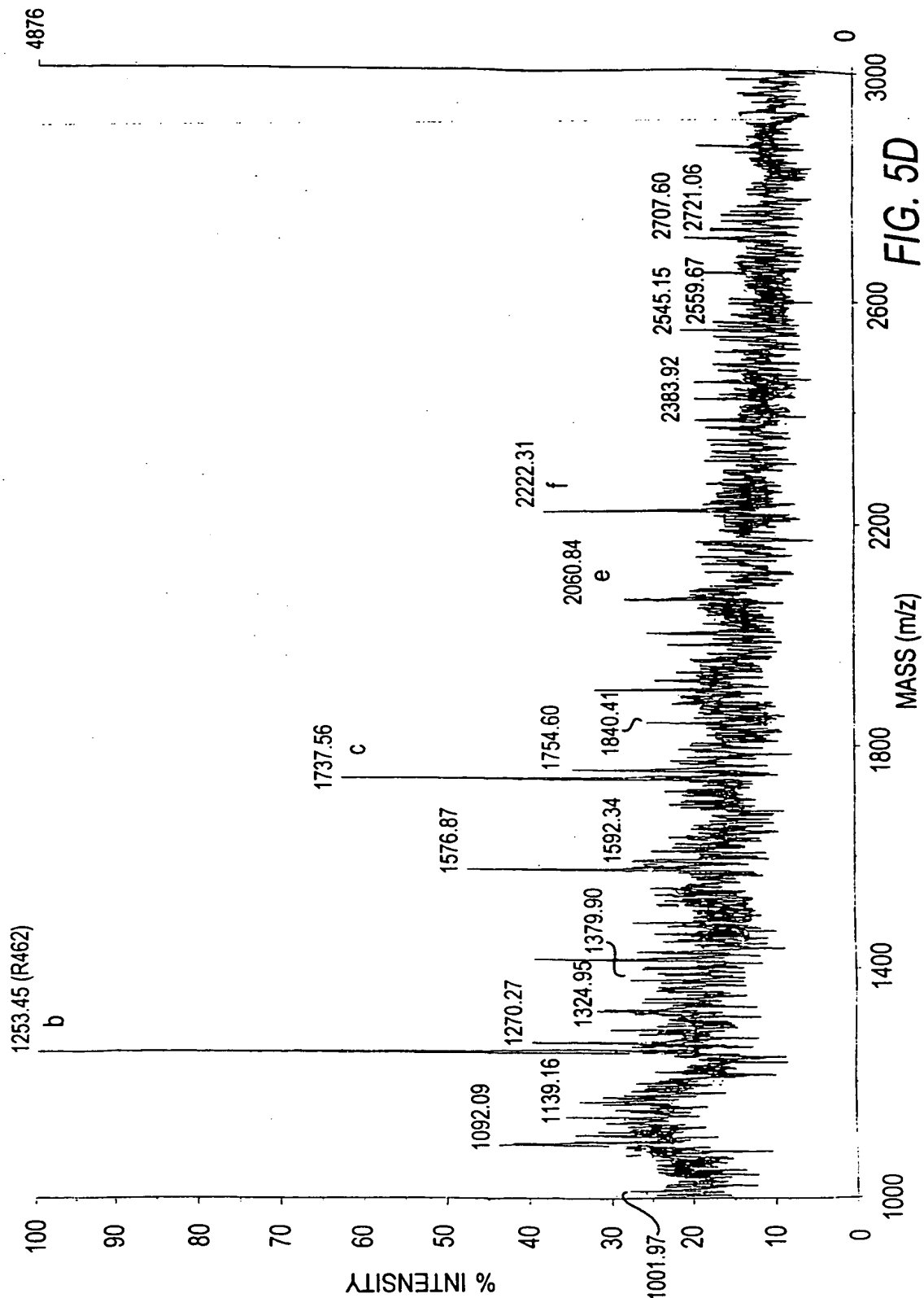


FIG. 5D

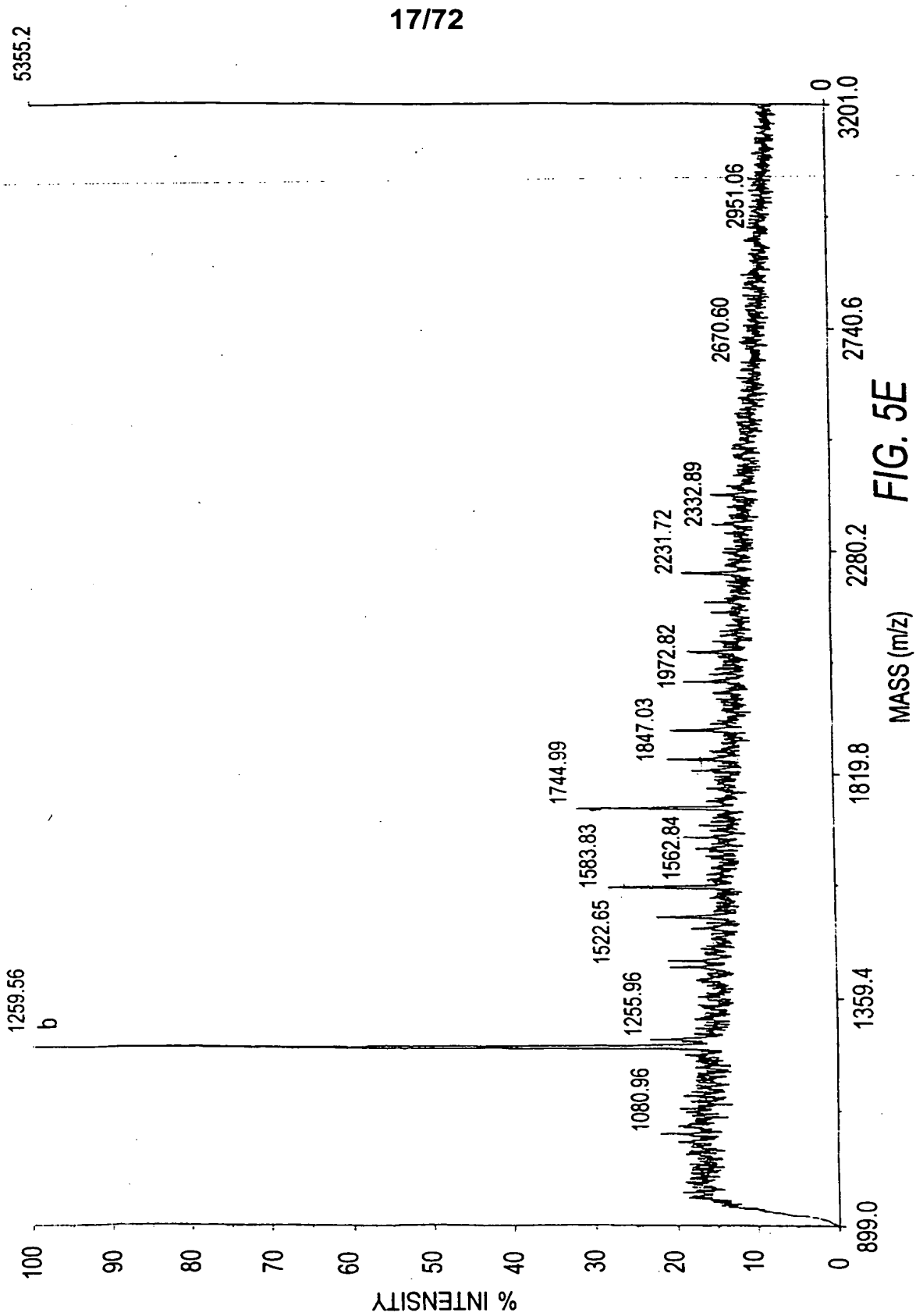


FIG. 5E

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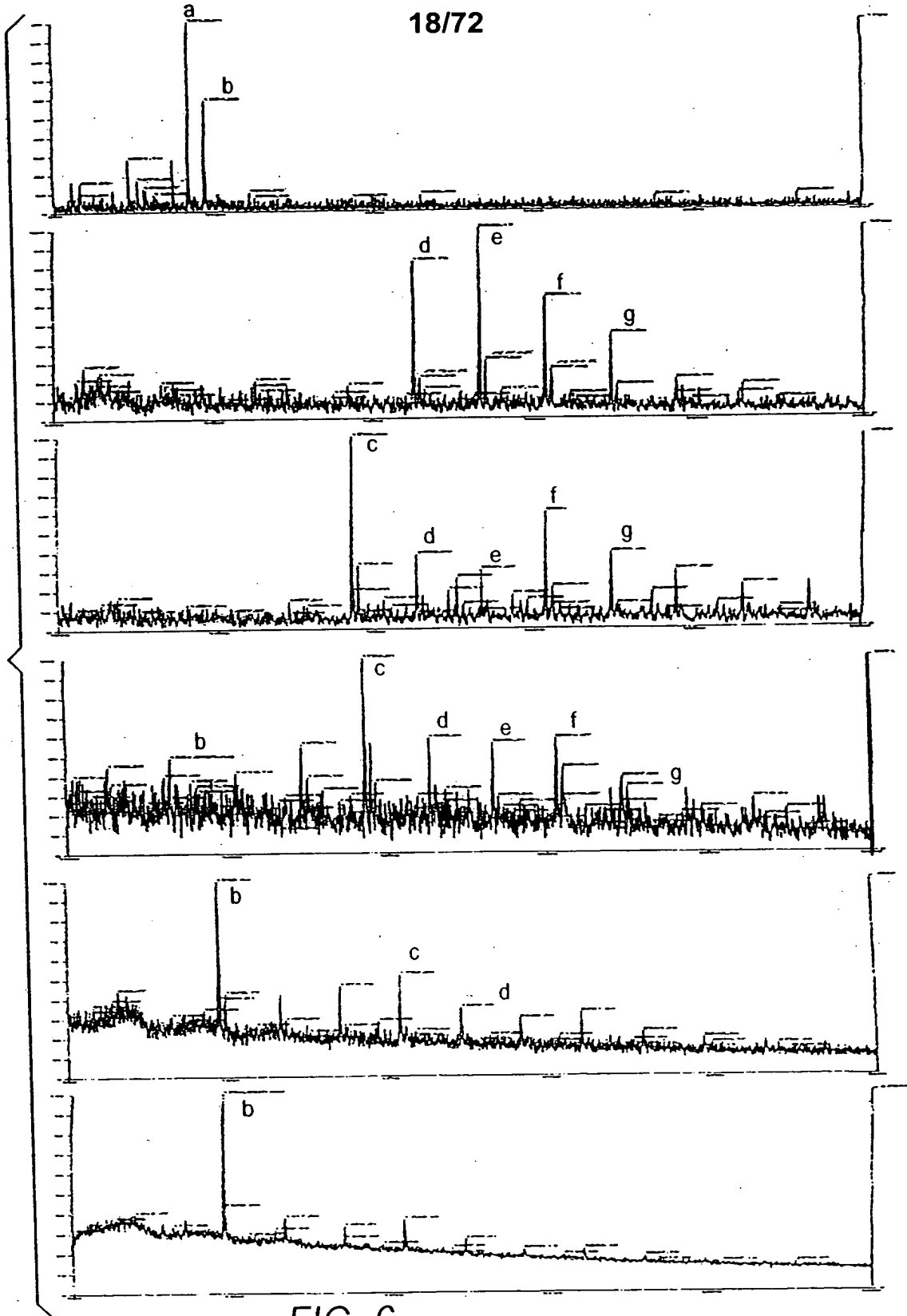
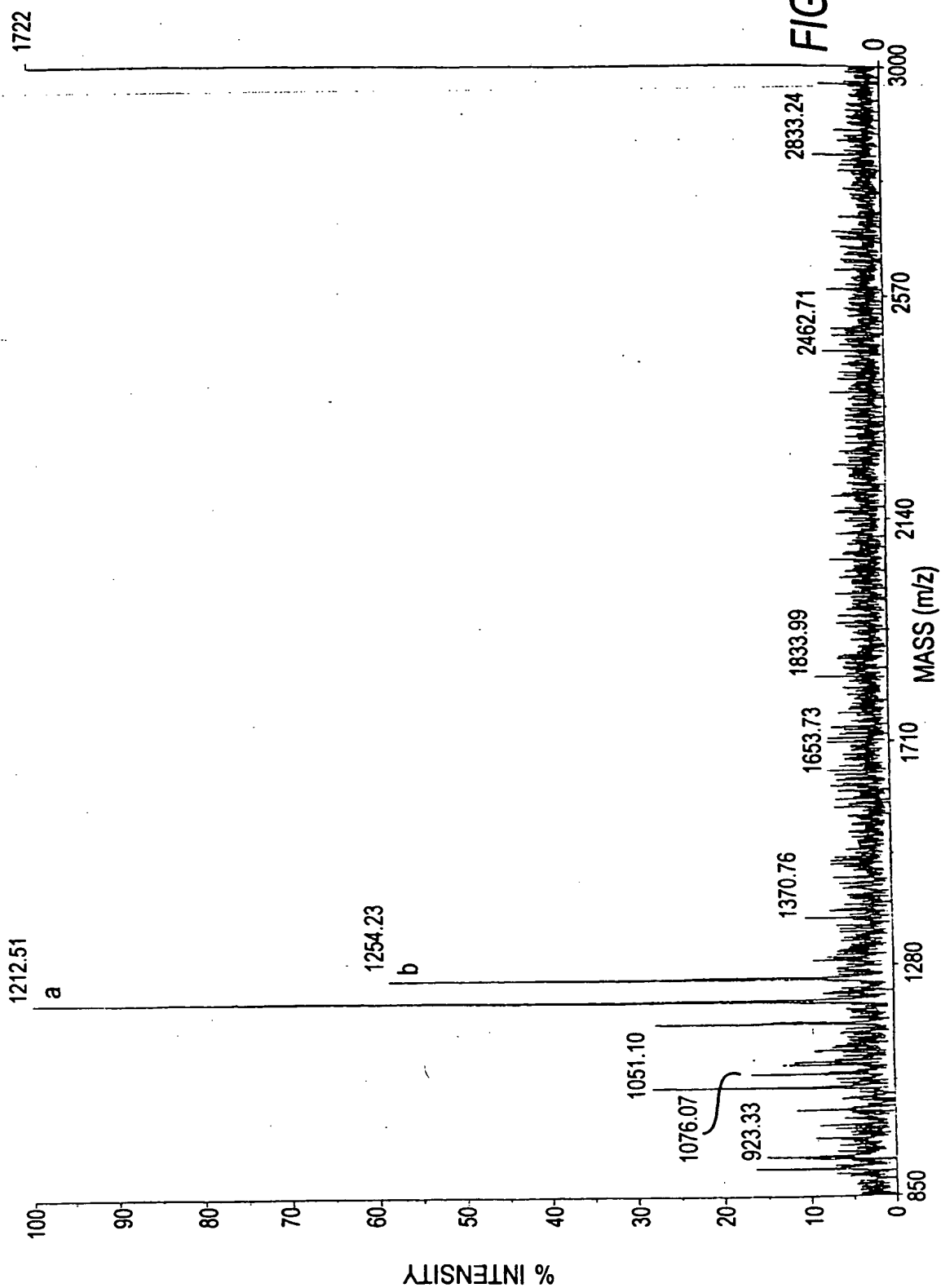


FIG. 6

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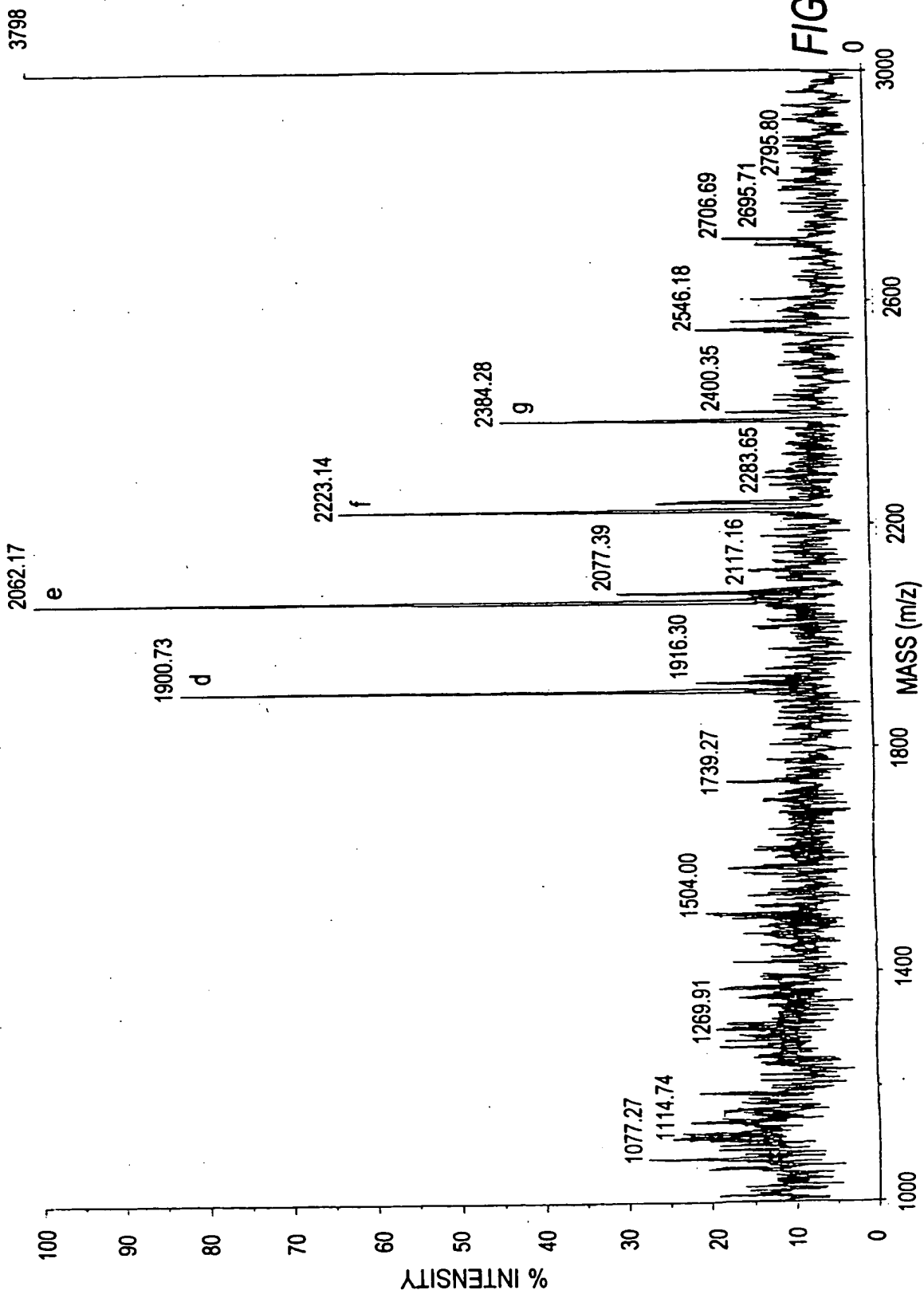


FIG. 6B

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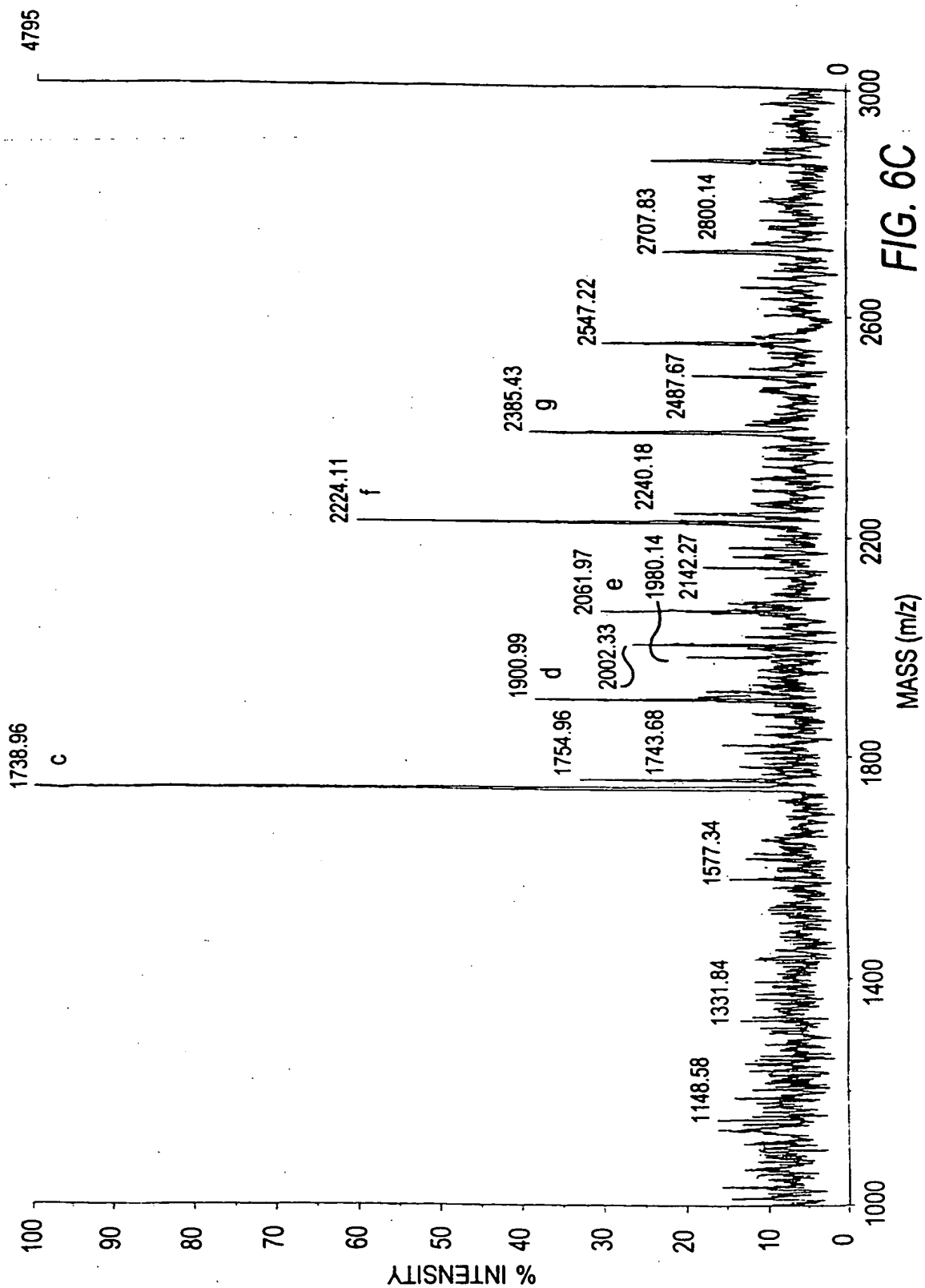


FIG. 6C

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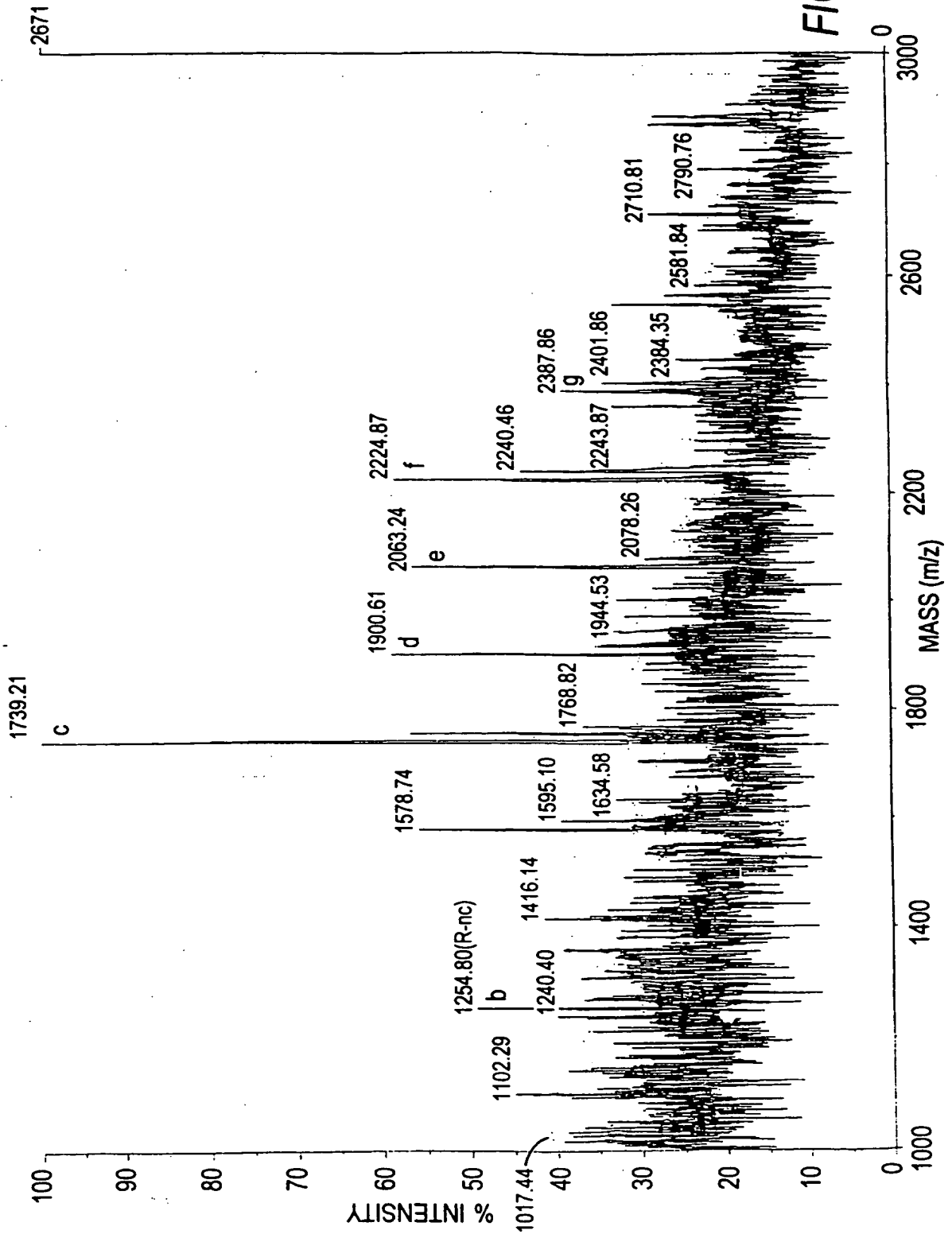


FIG. 6D

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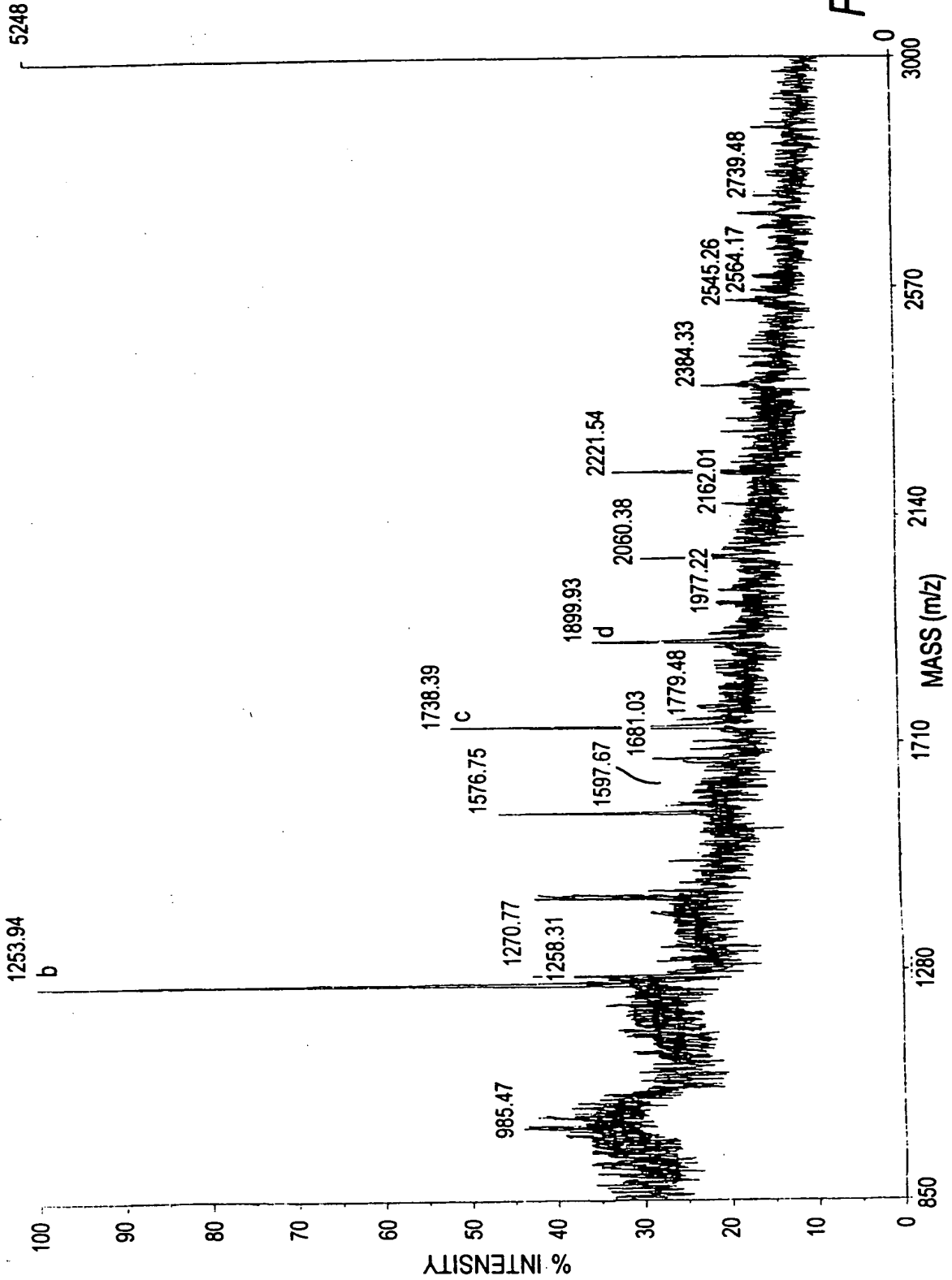
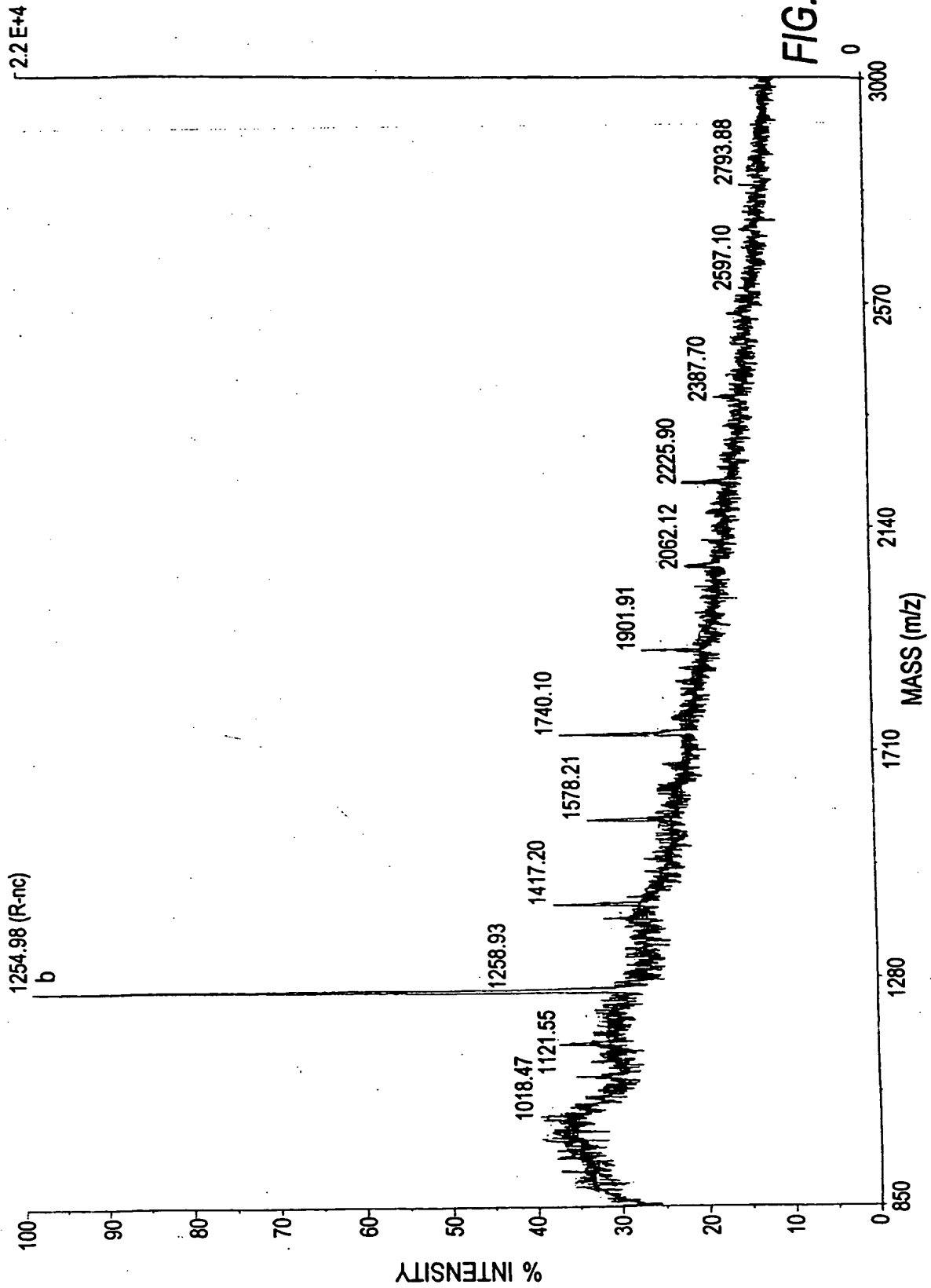


FIG. 6E



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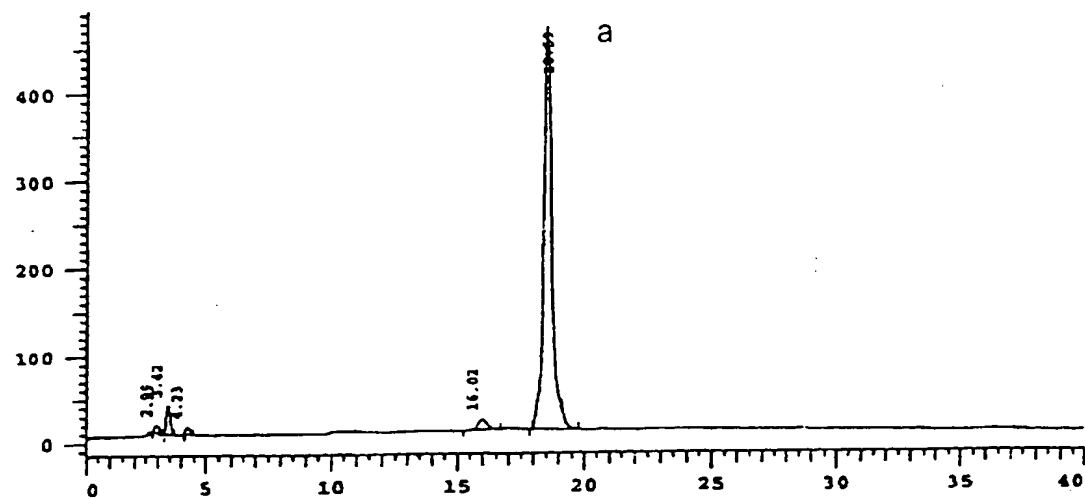
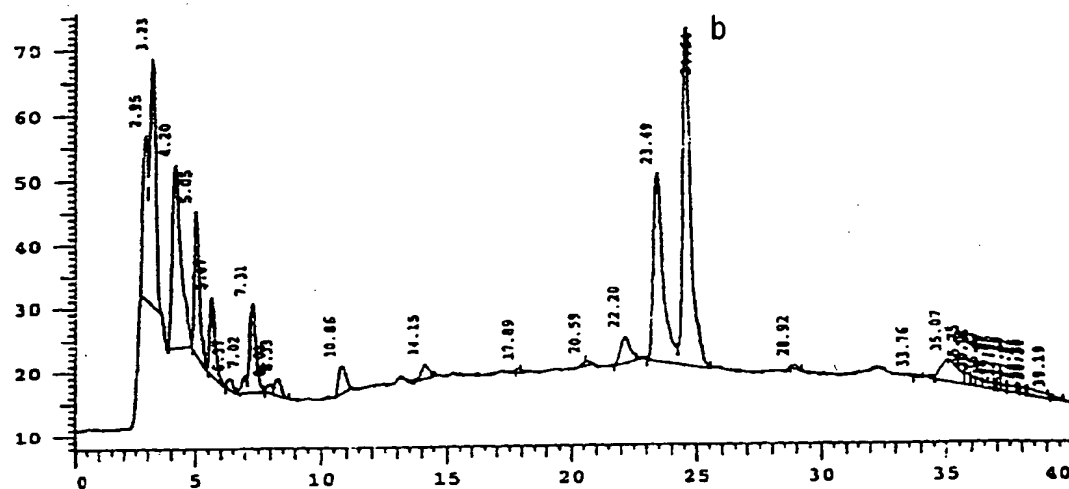
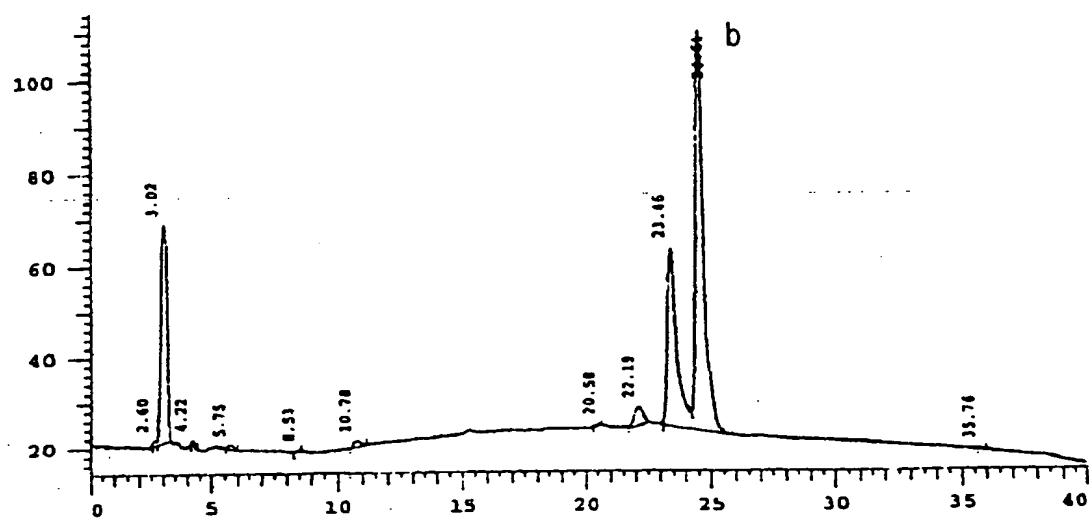


FIG. 7

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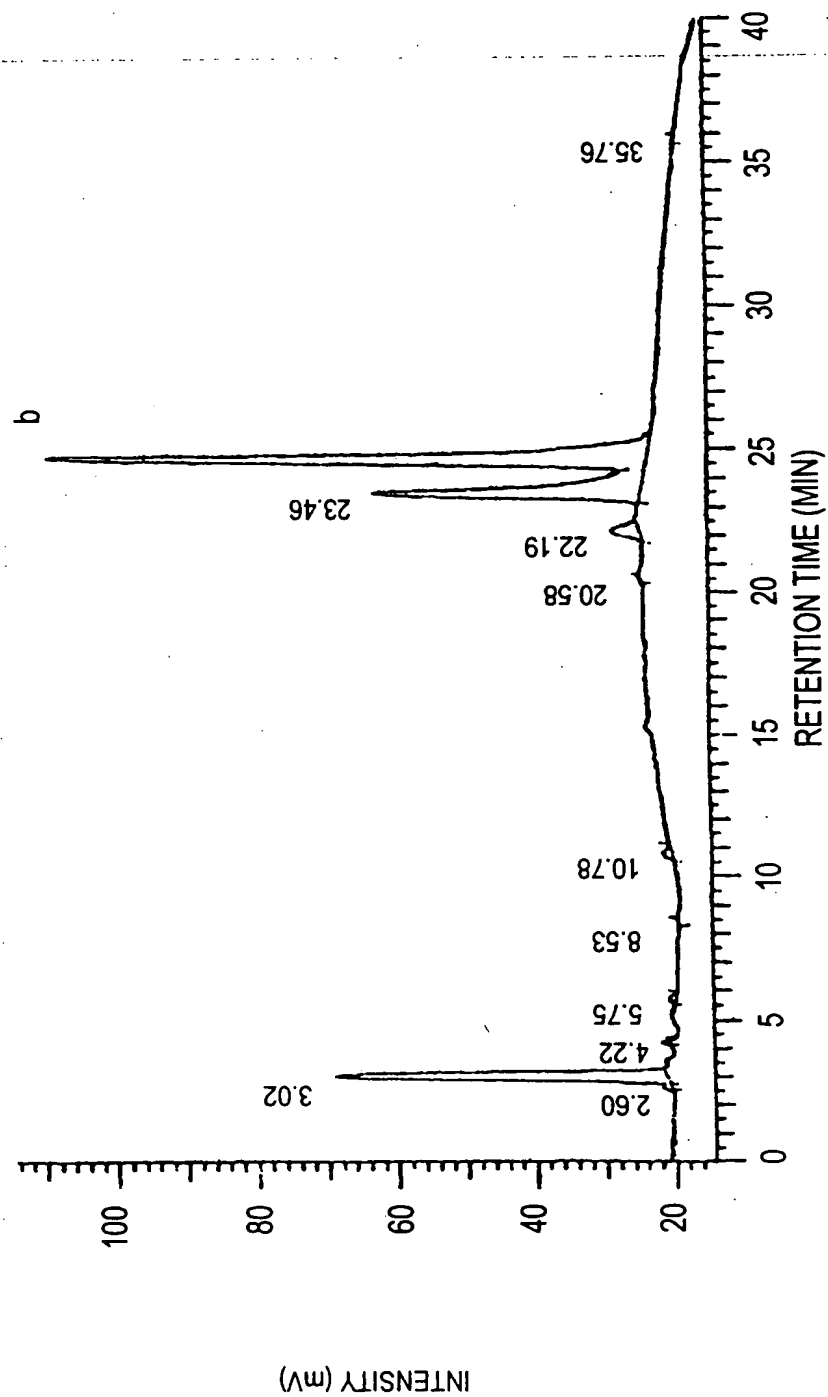


FIG. 7A

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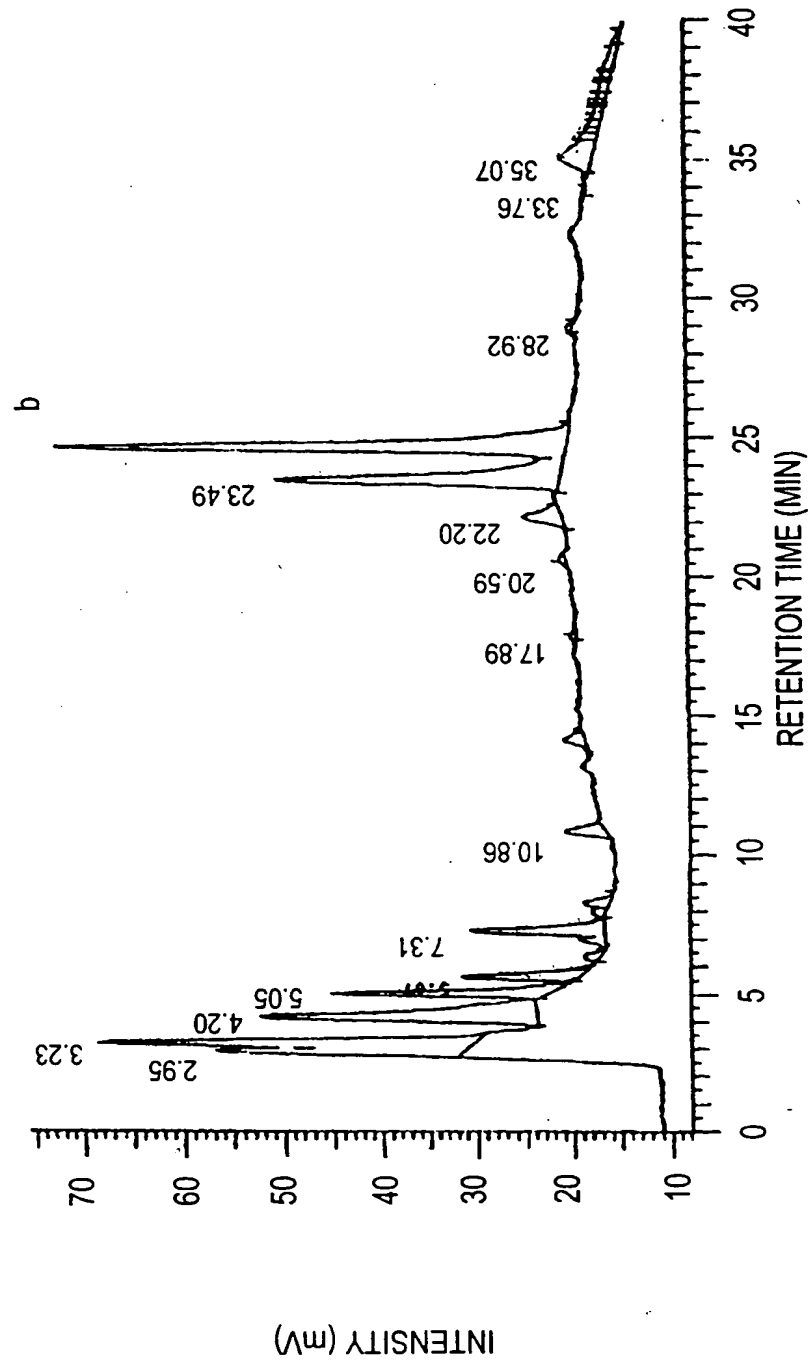


FIG. 7B

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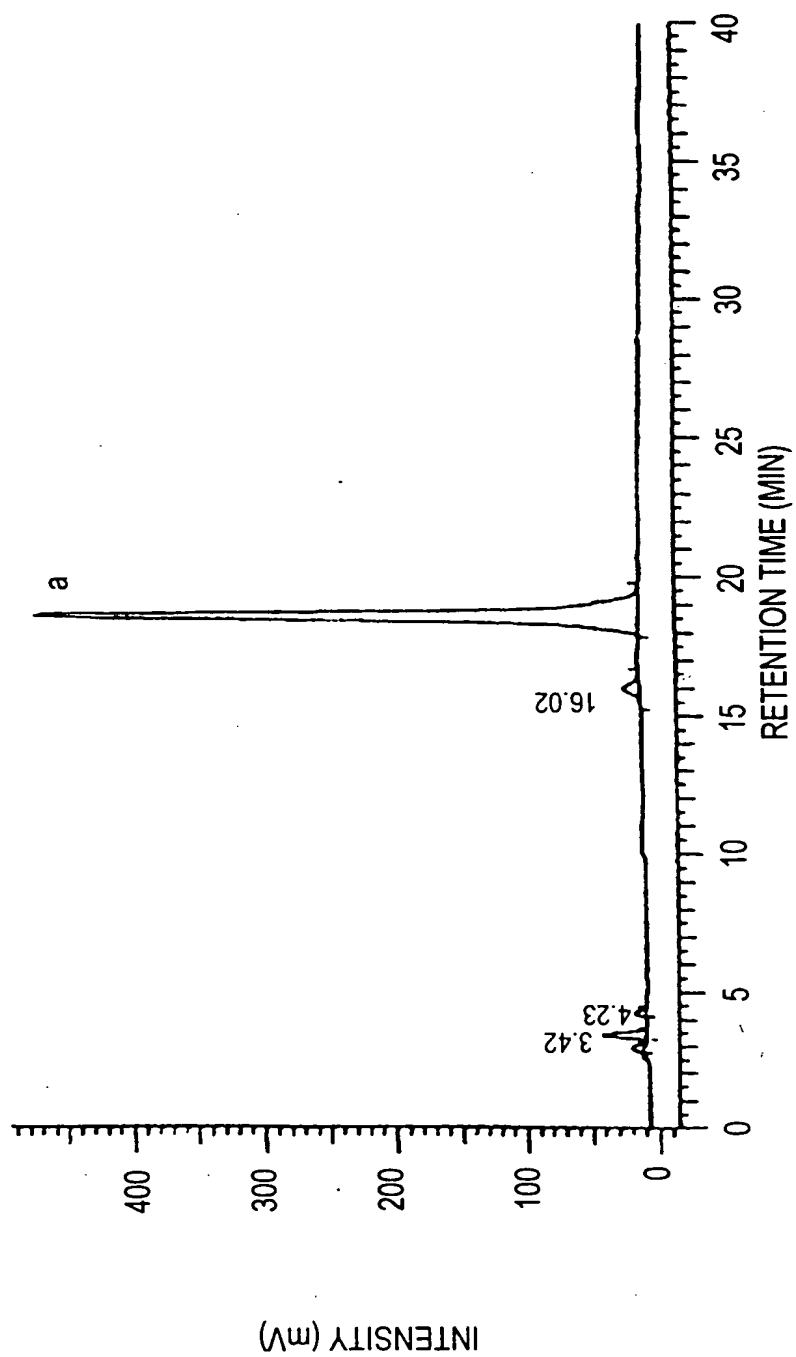


FIG. 7C

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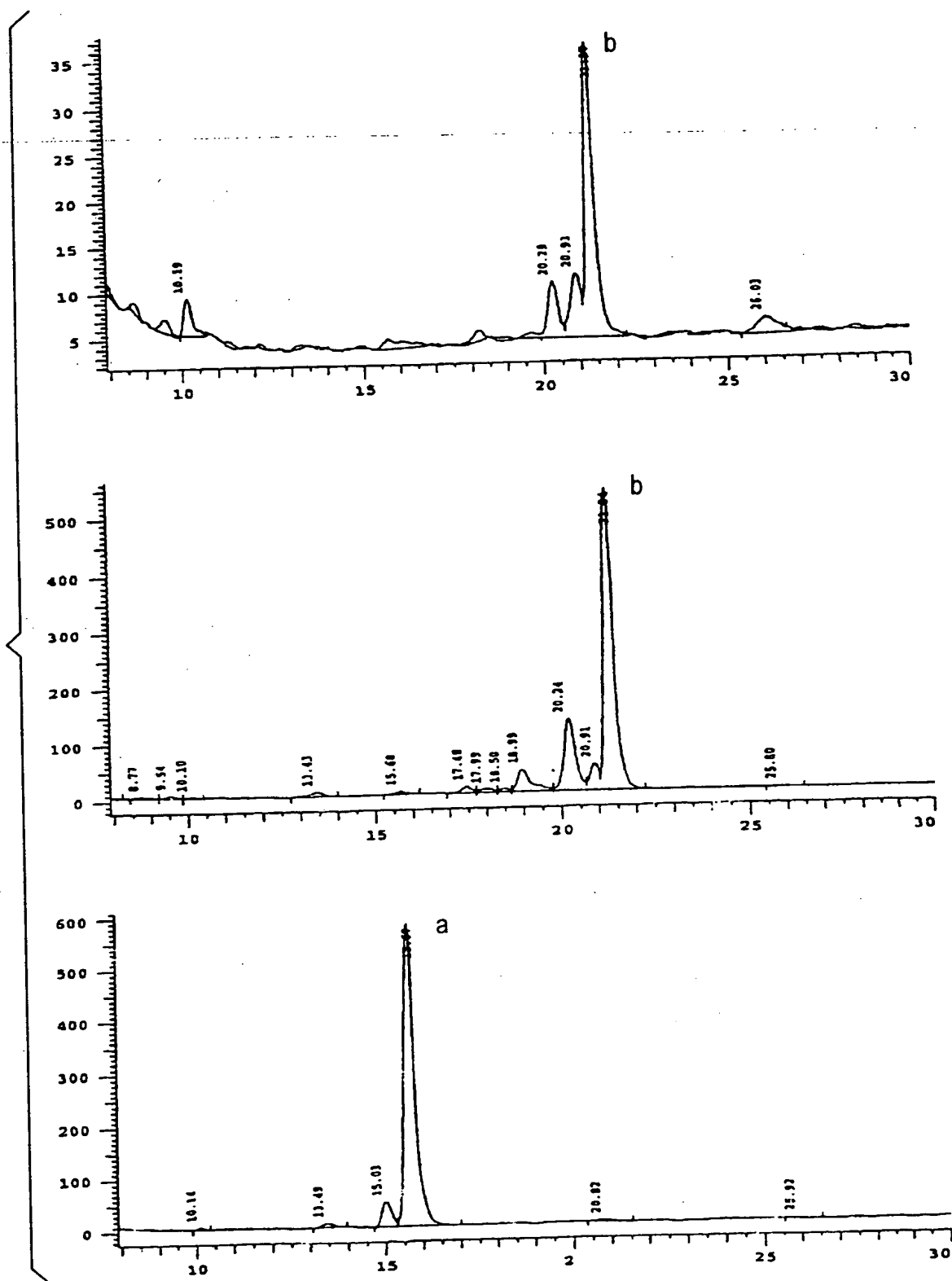


FIG. 8

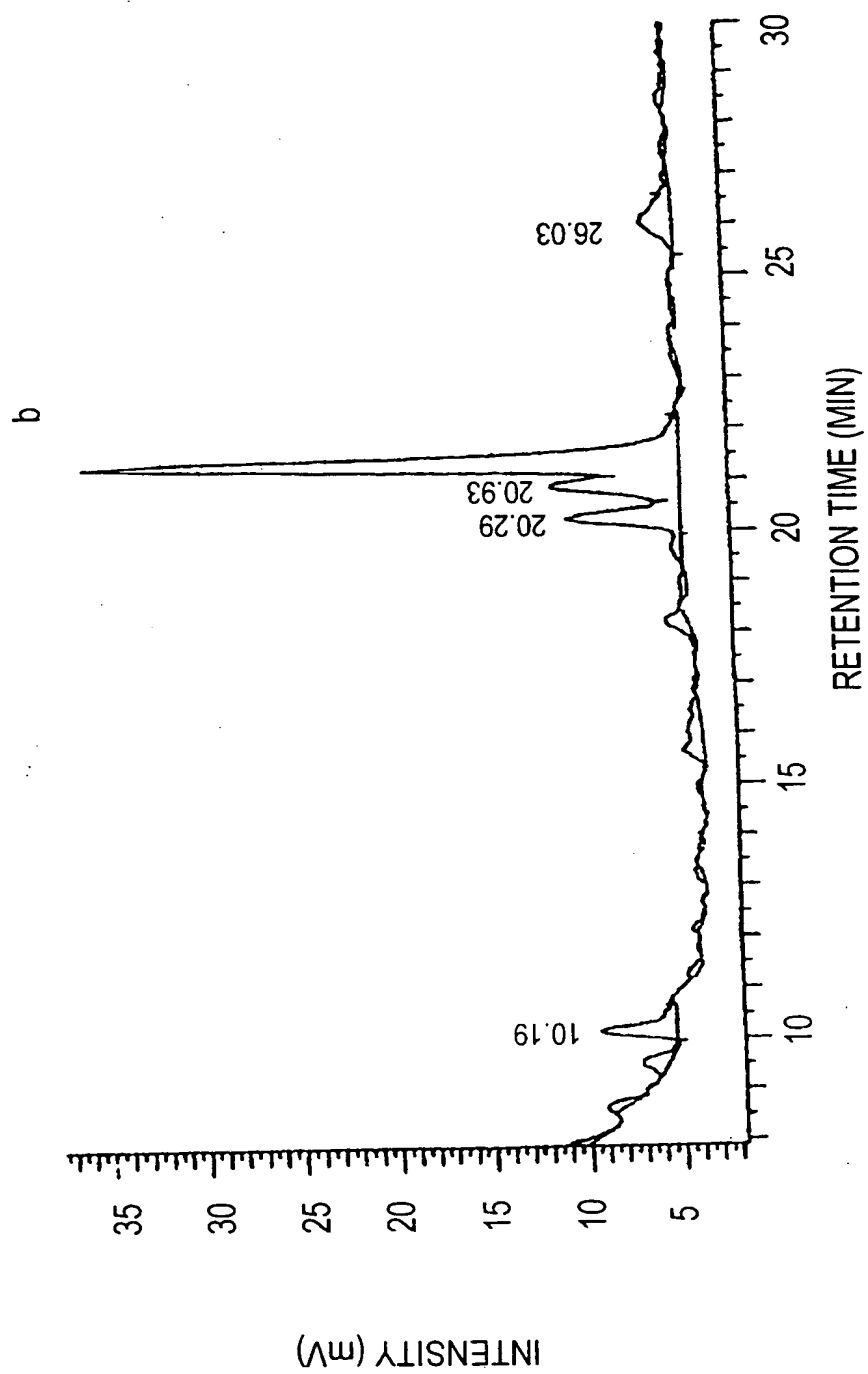


FIG. 8A

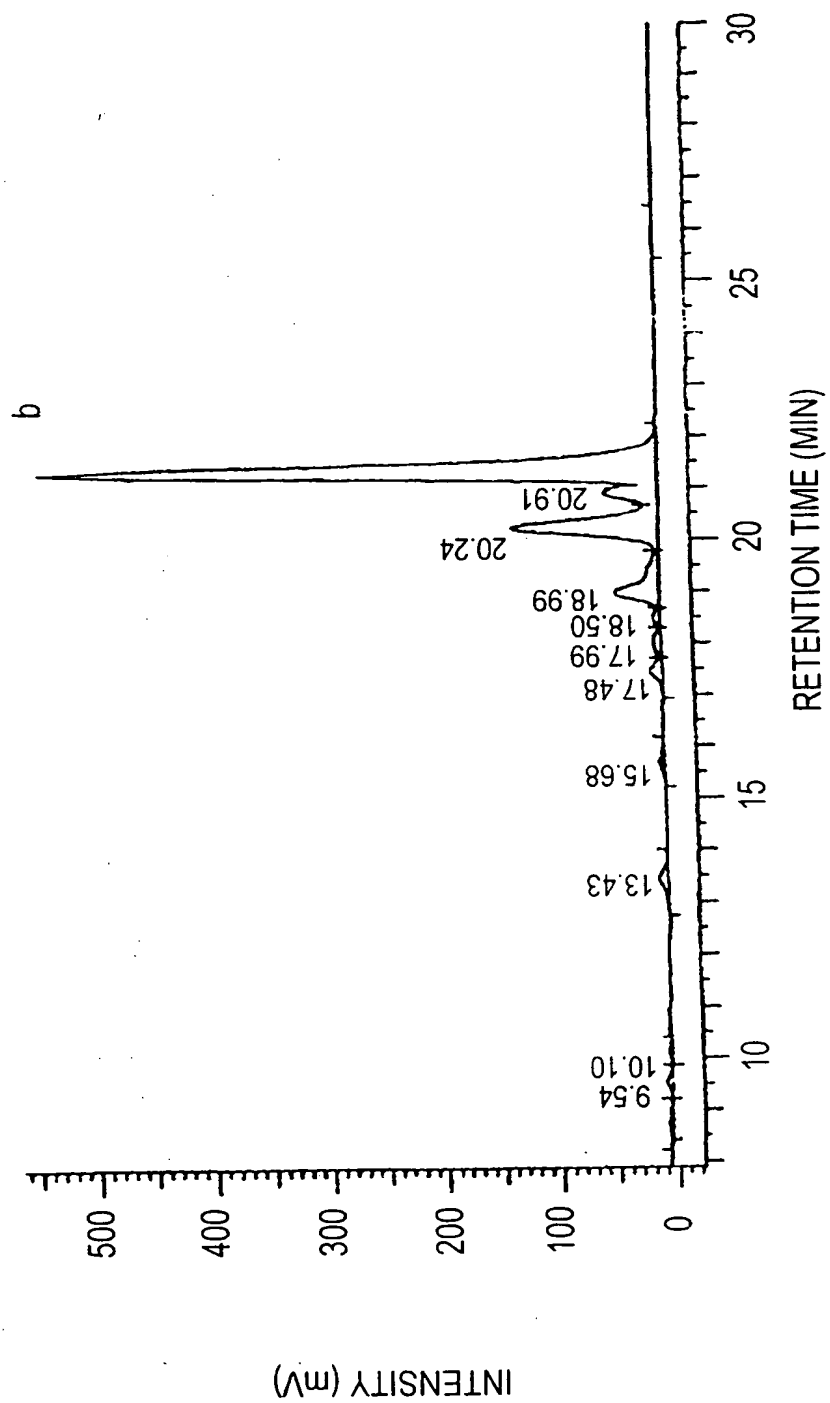


FIG. 8B

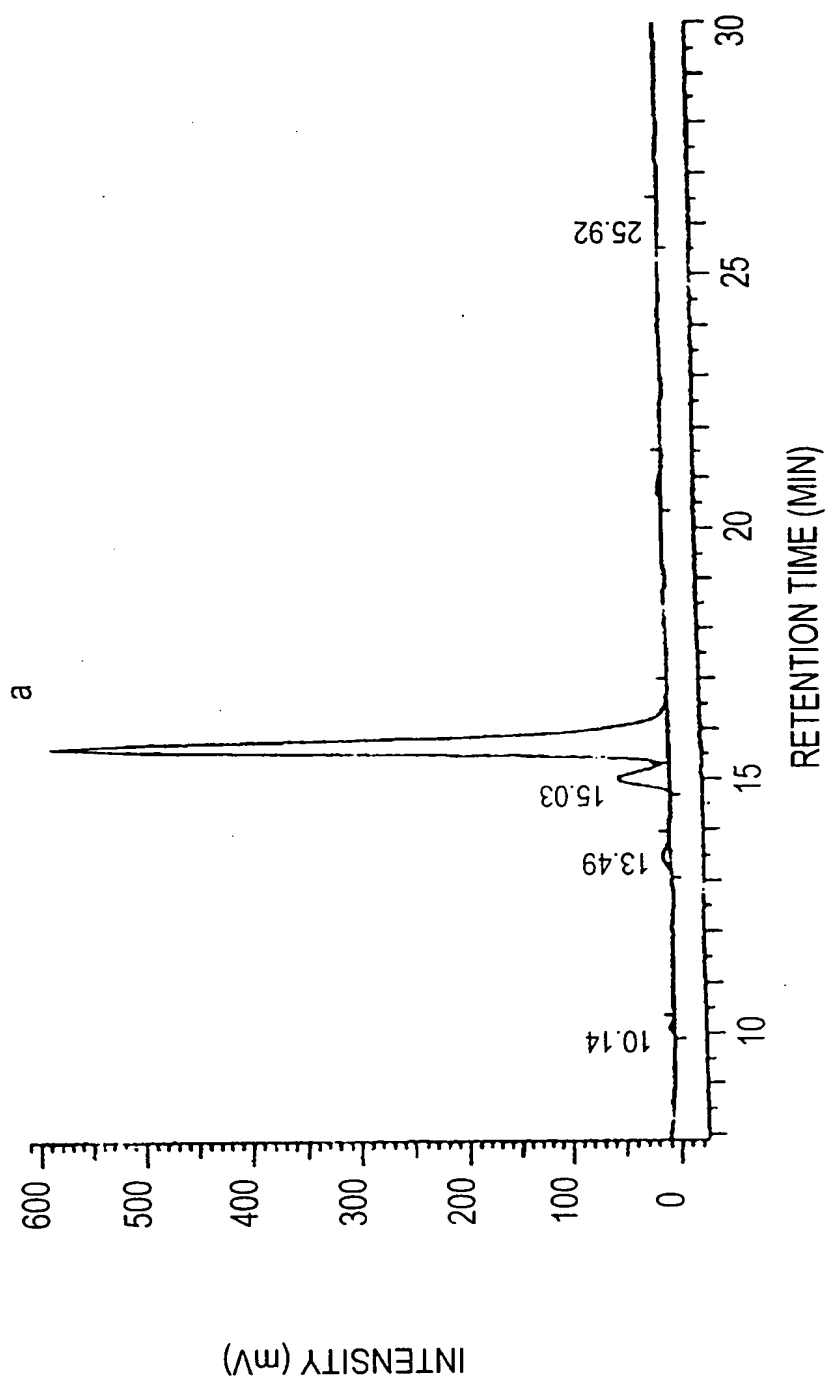


FIG. 8C

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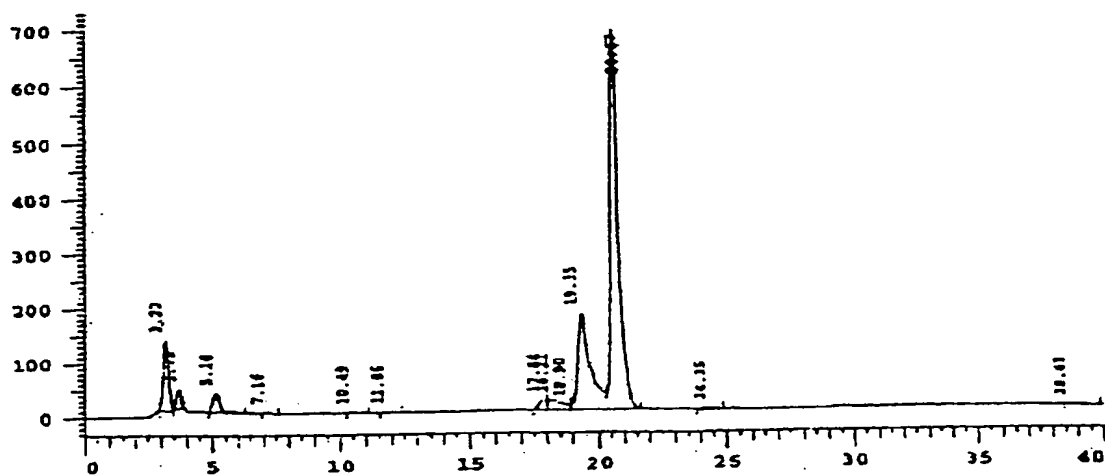
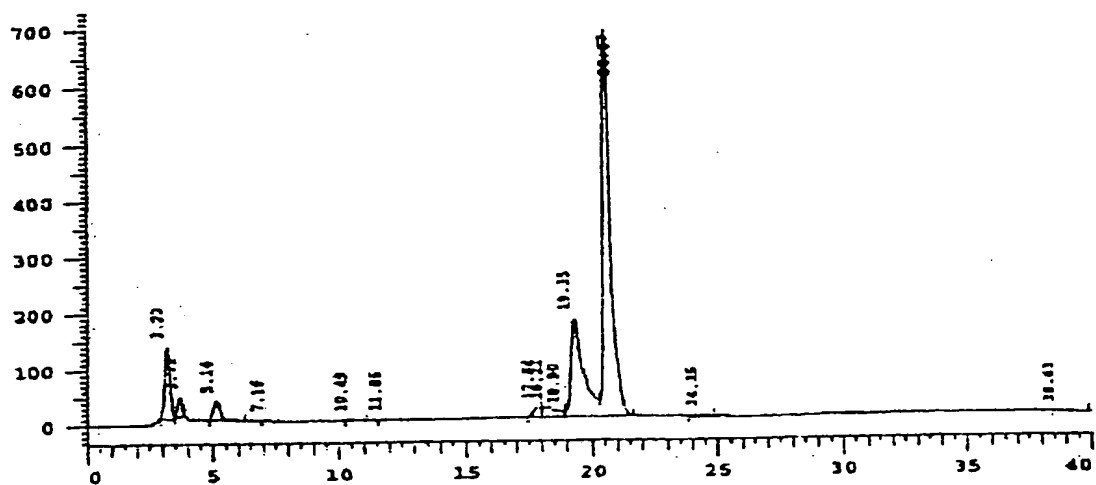
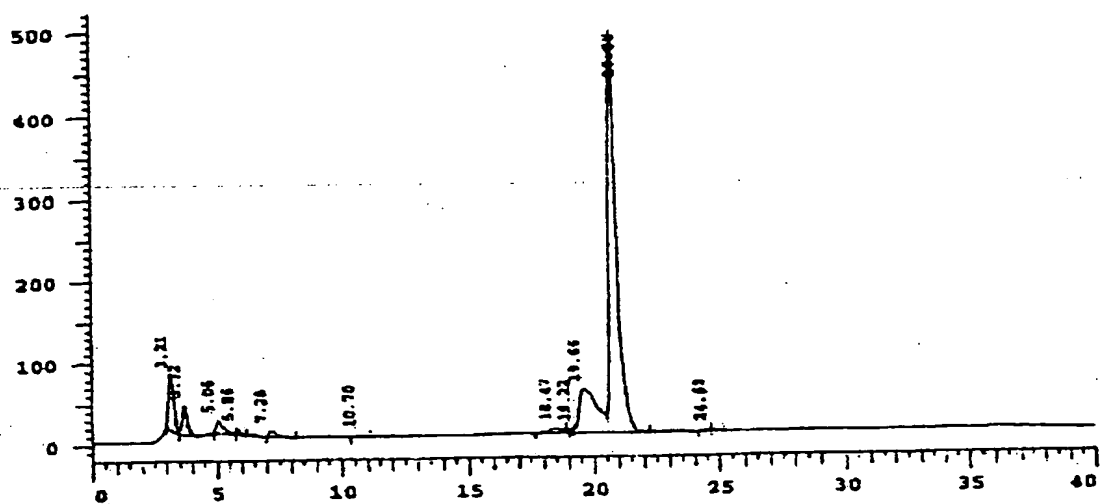


FIG. 9

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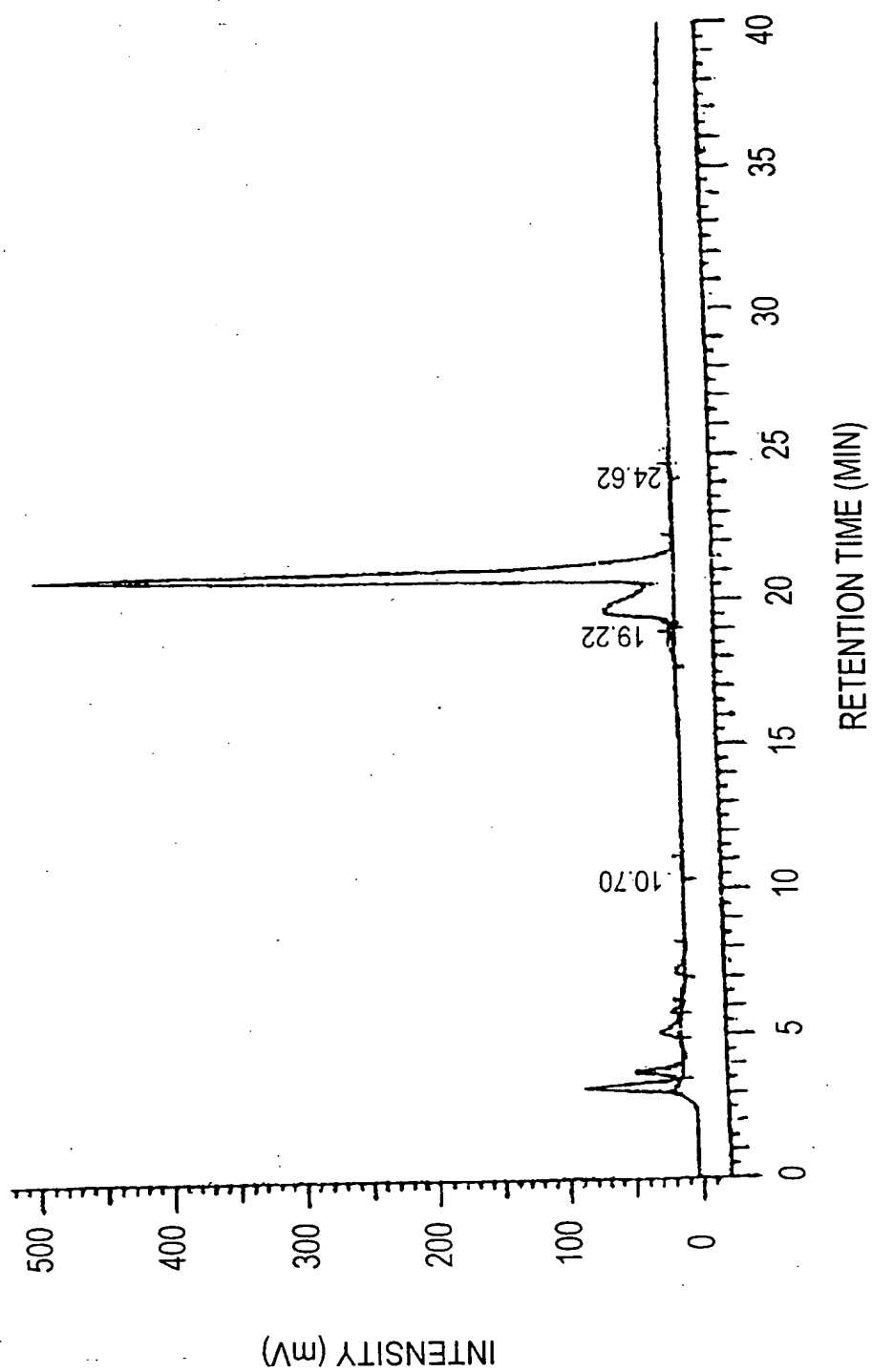


FIG. 9A

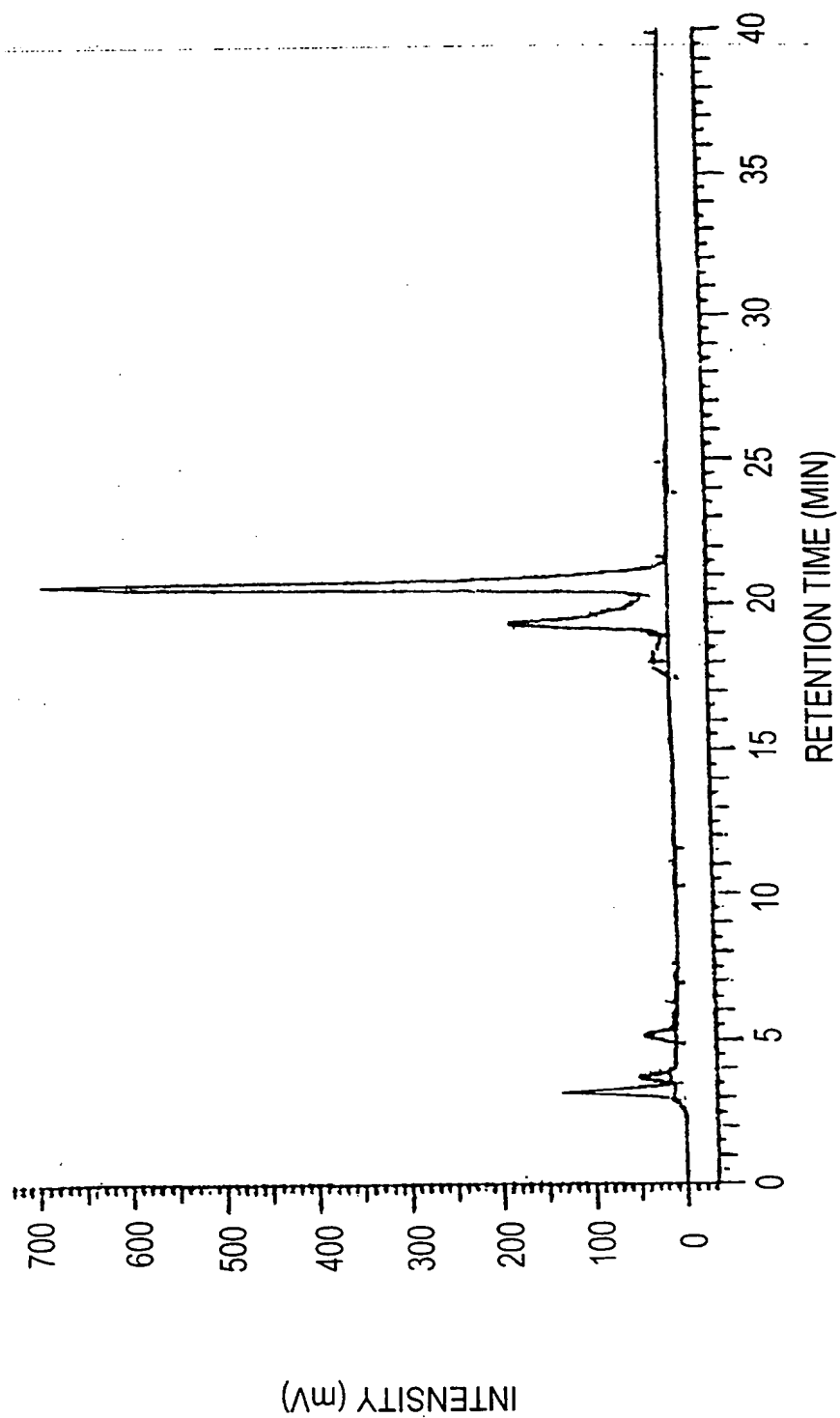


FIG. 9B

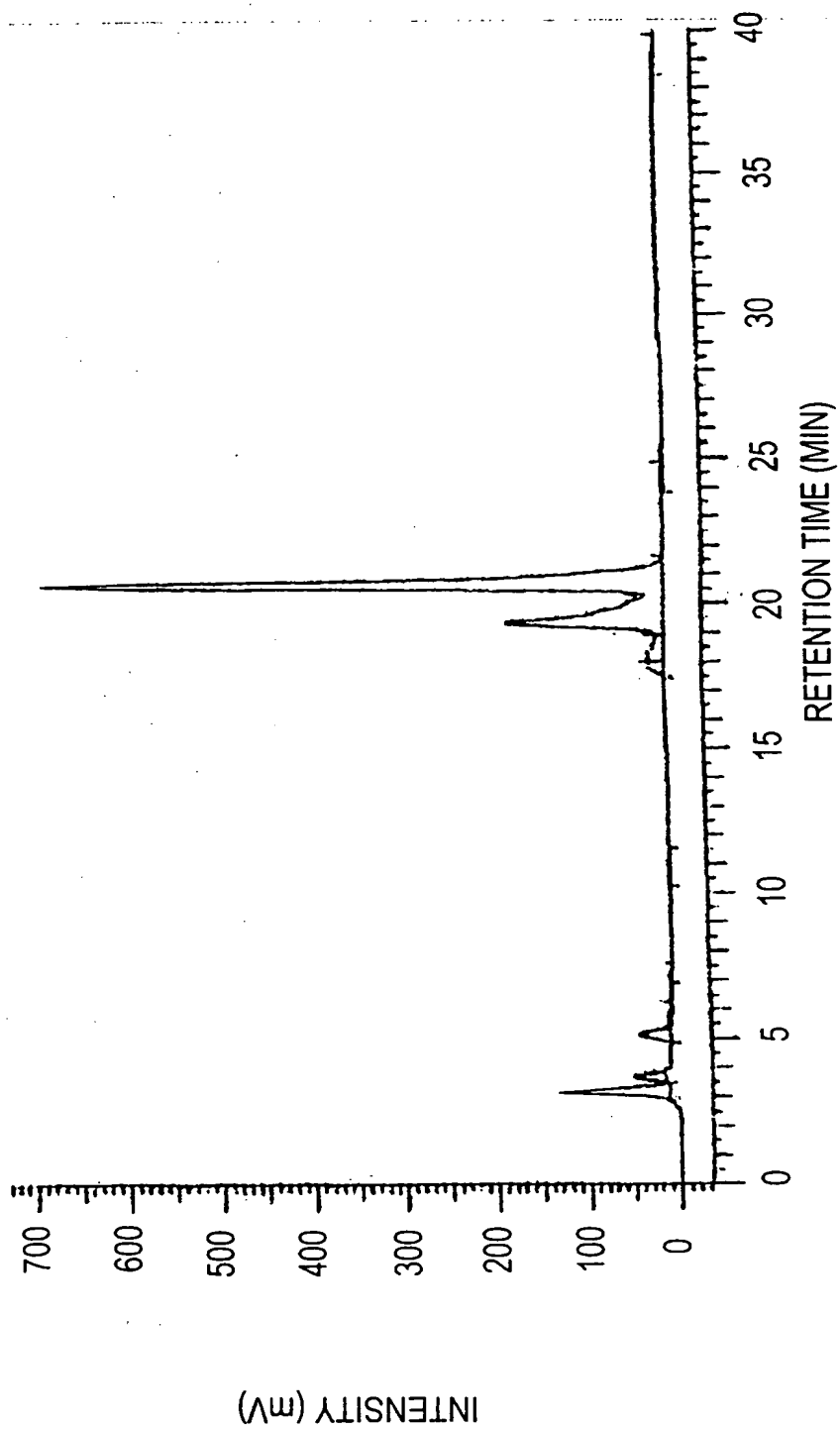


FIG. 9C

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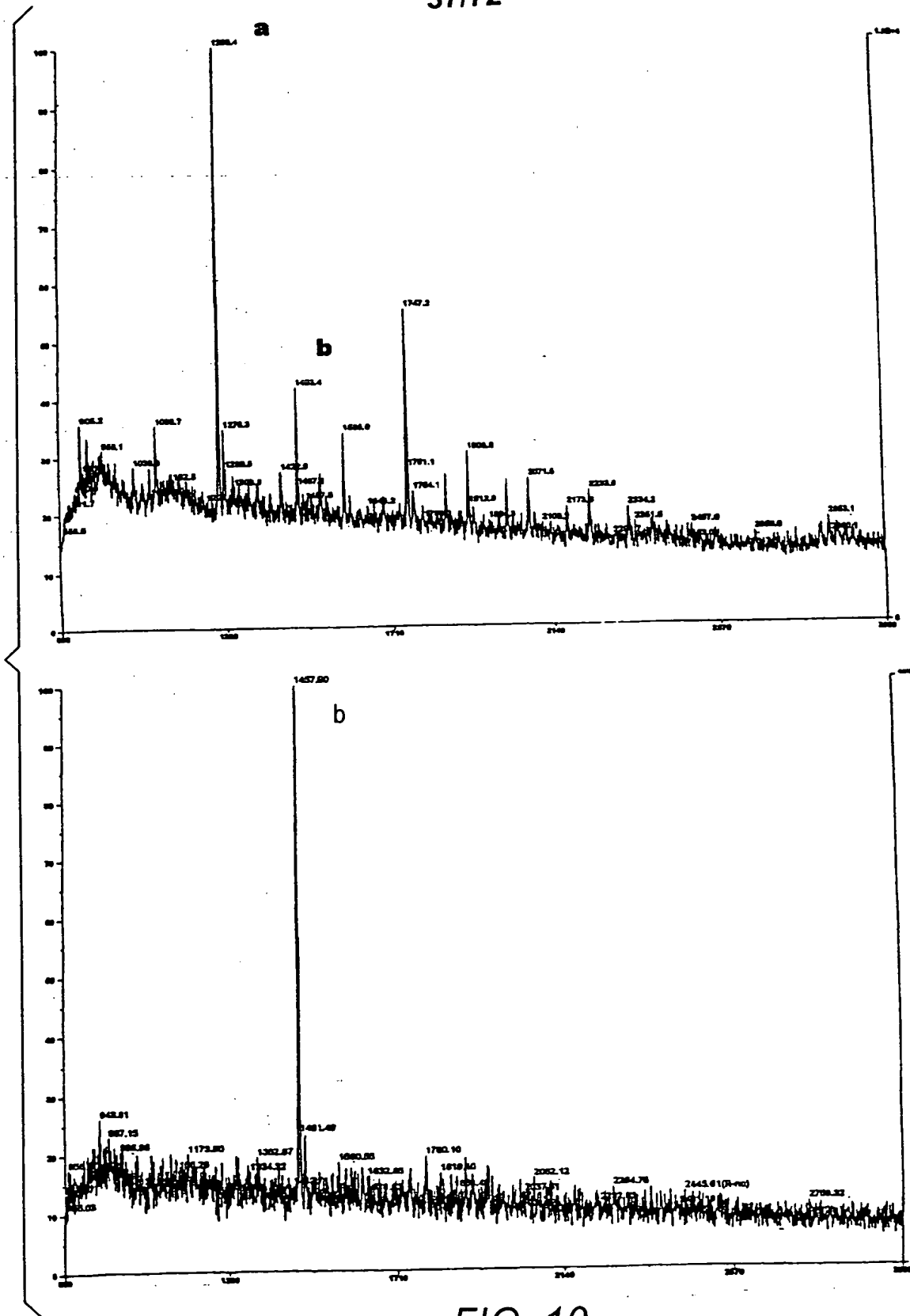
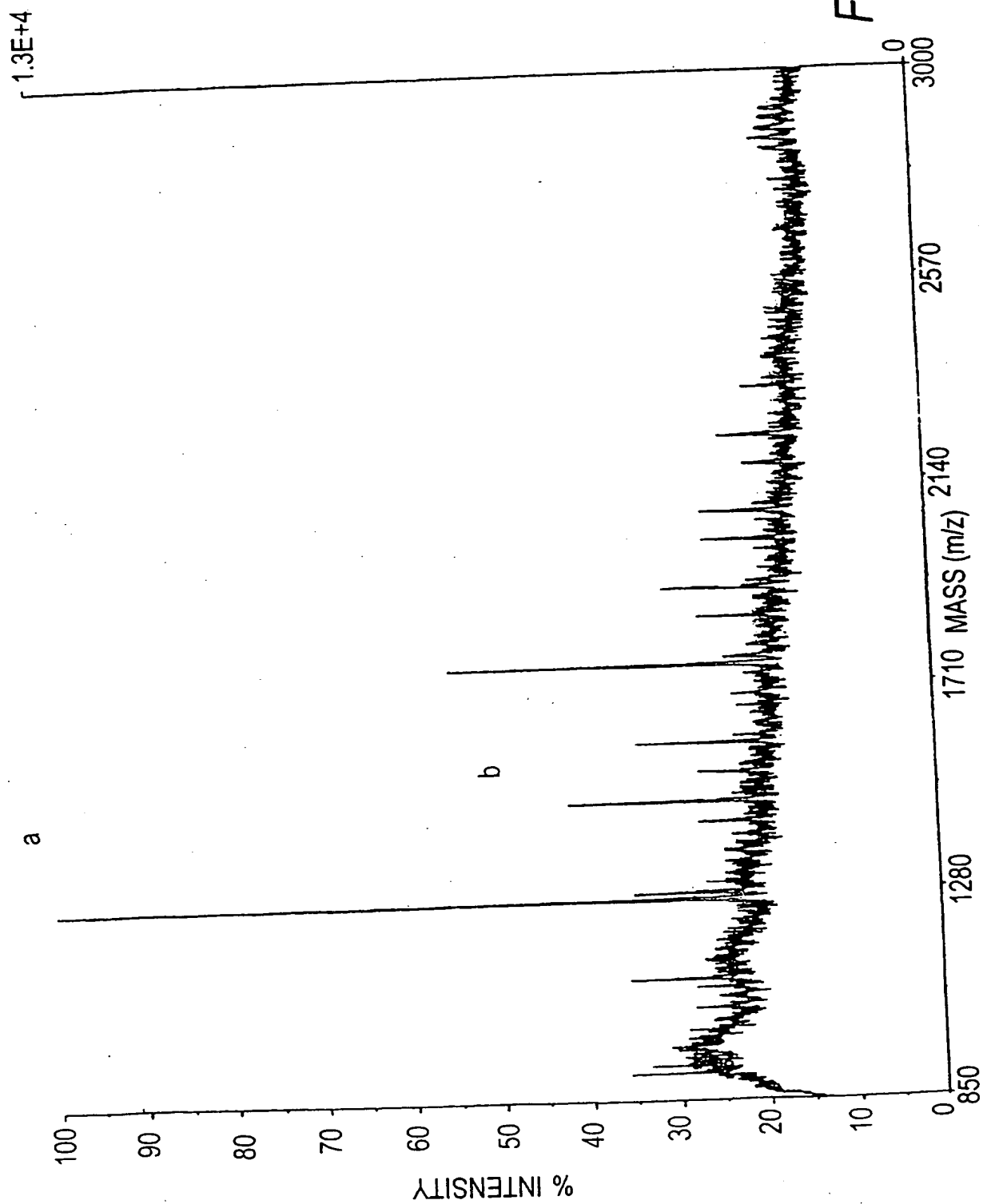


FIG. 10



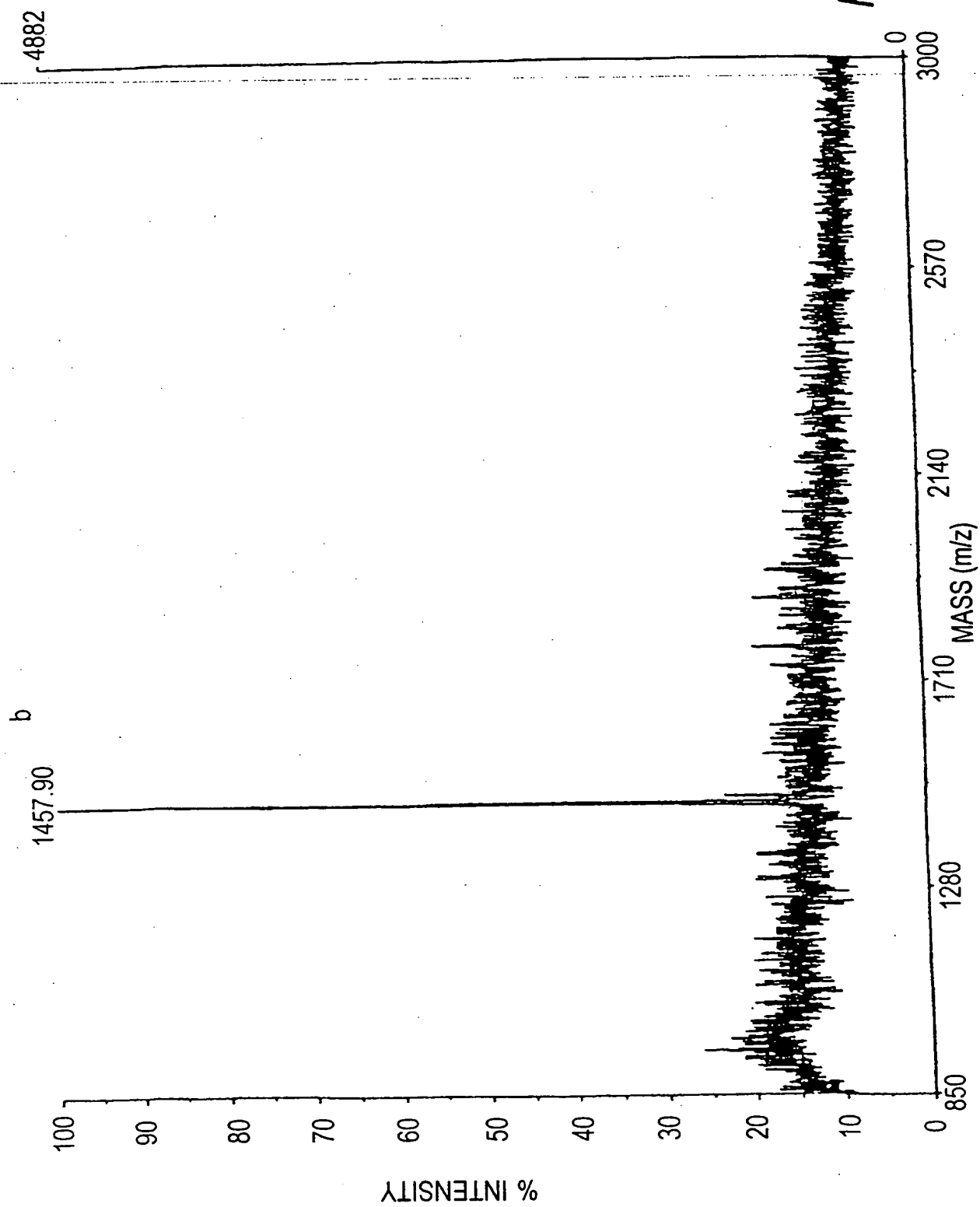


FIG. 10B

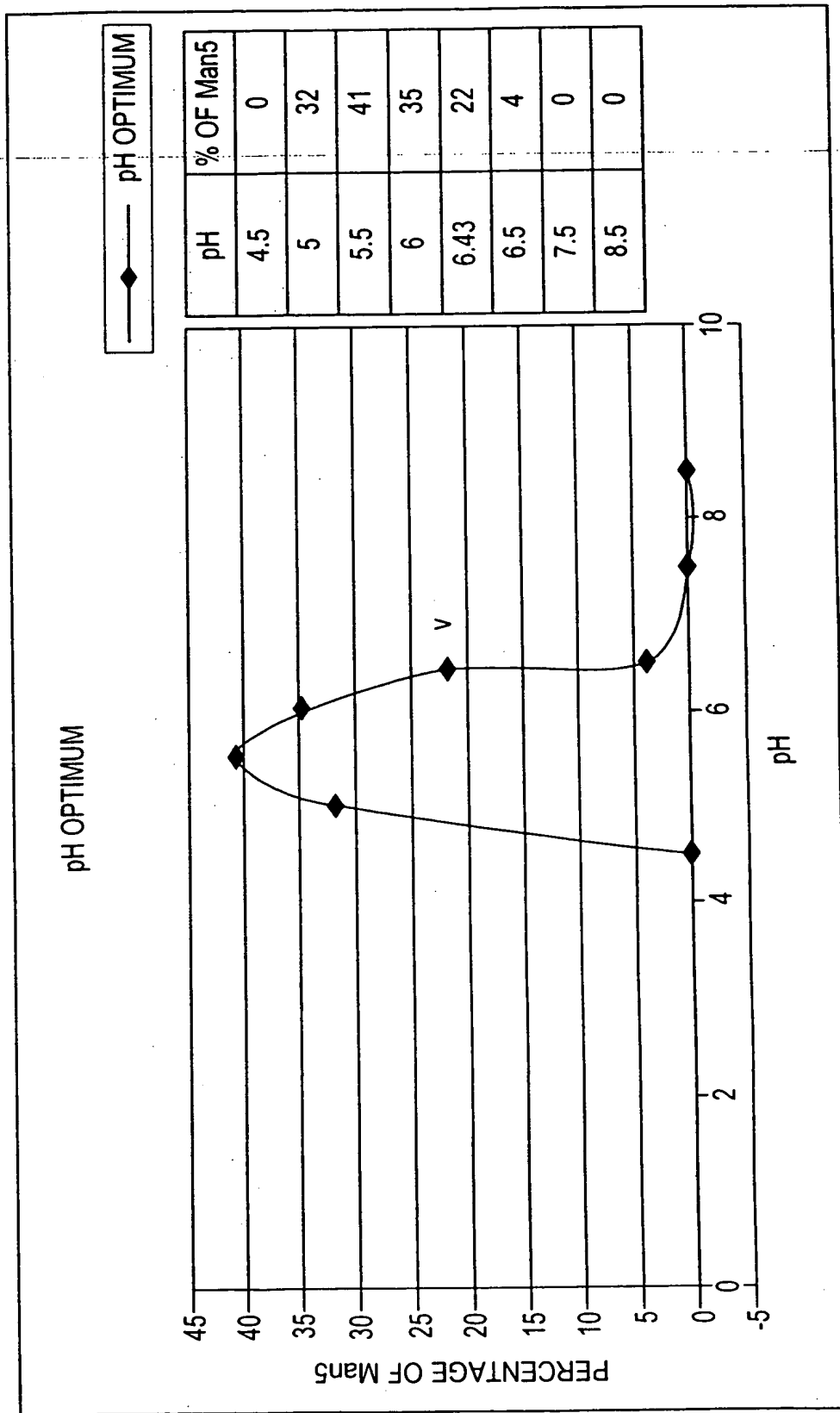


FIG. 11

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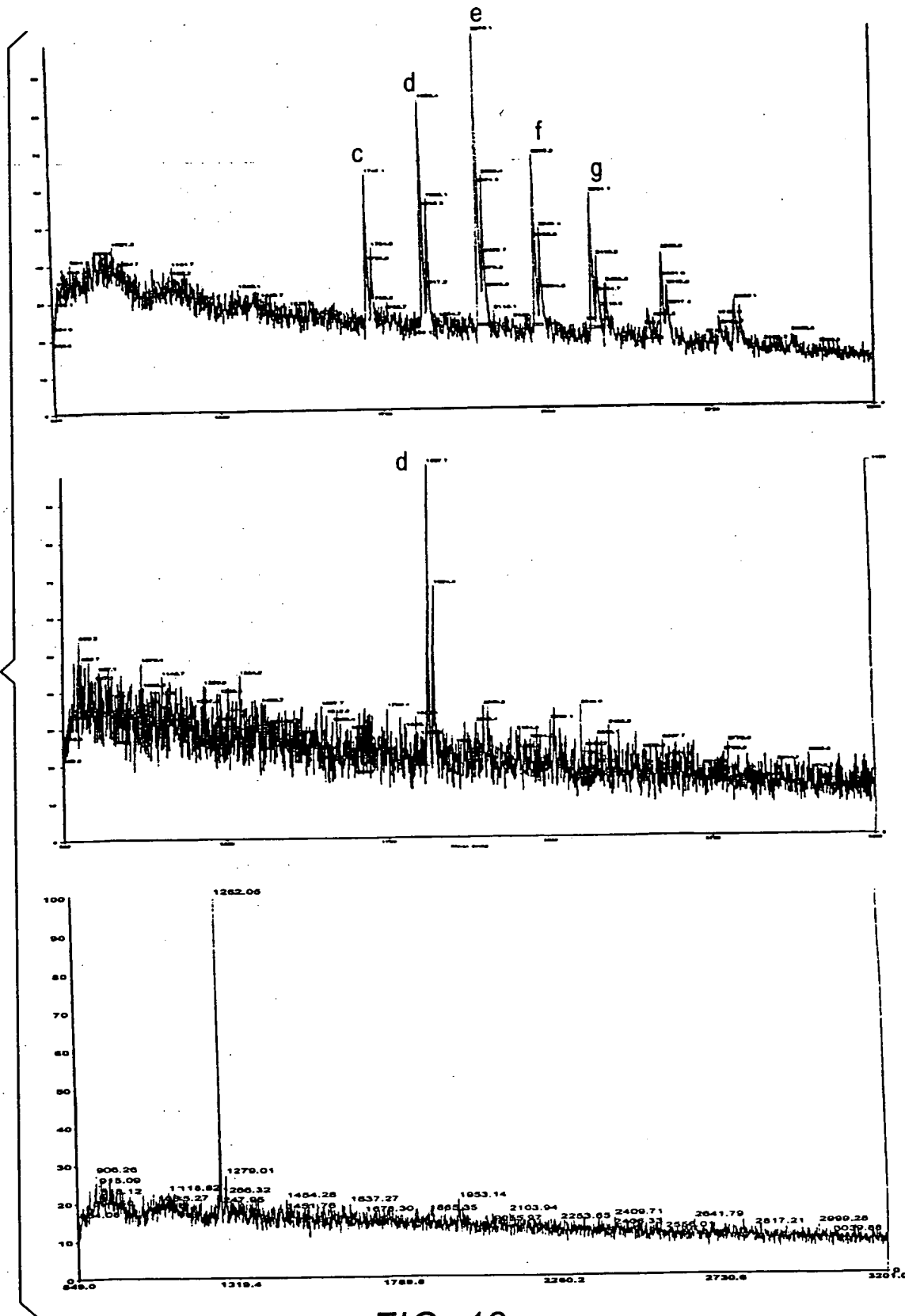
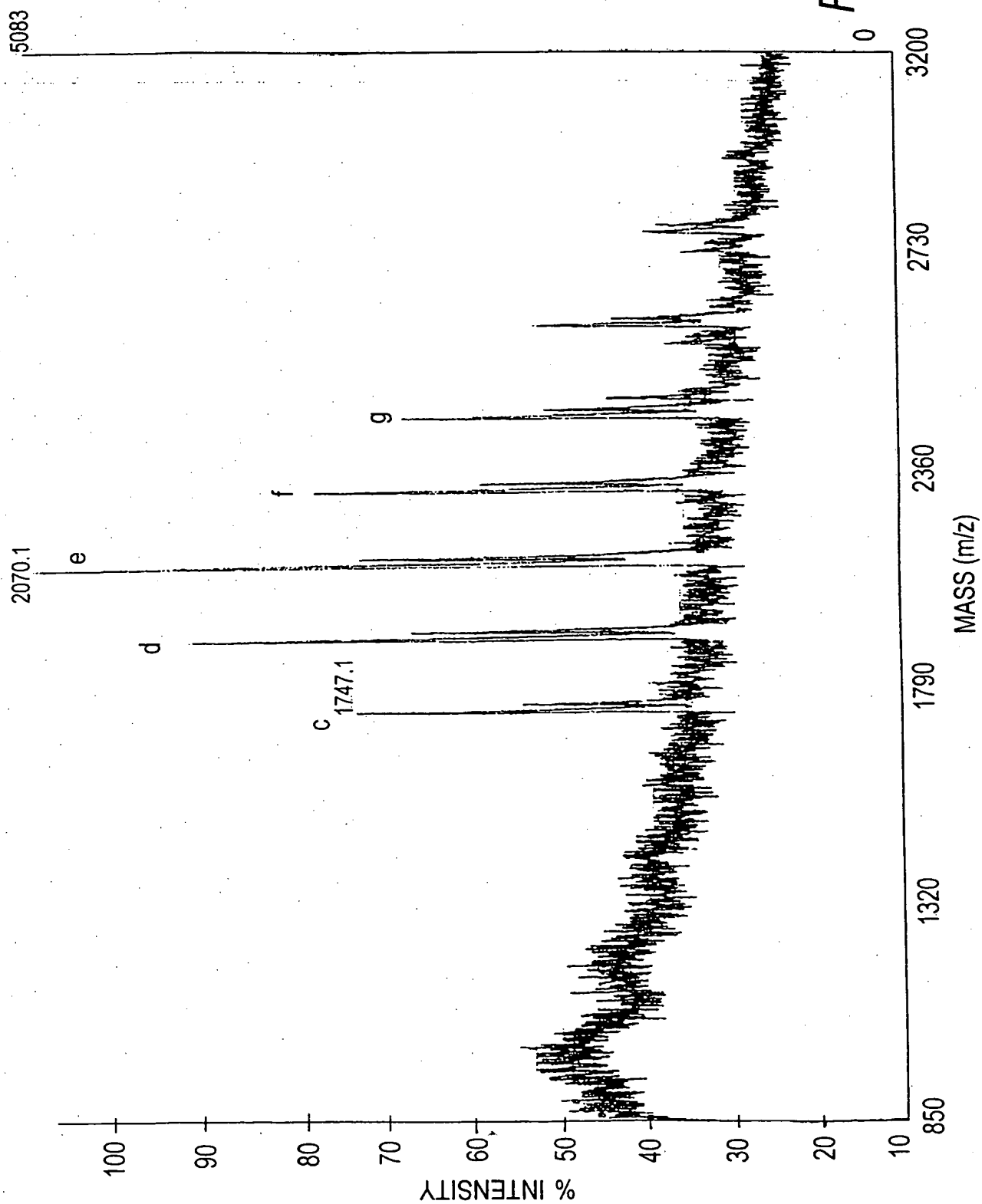


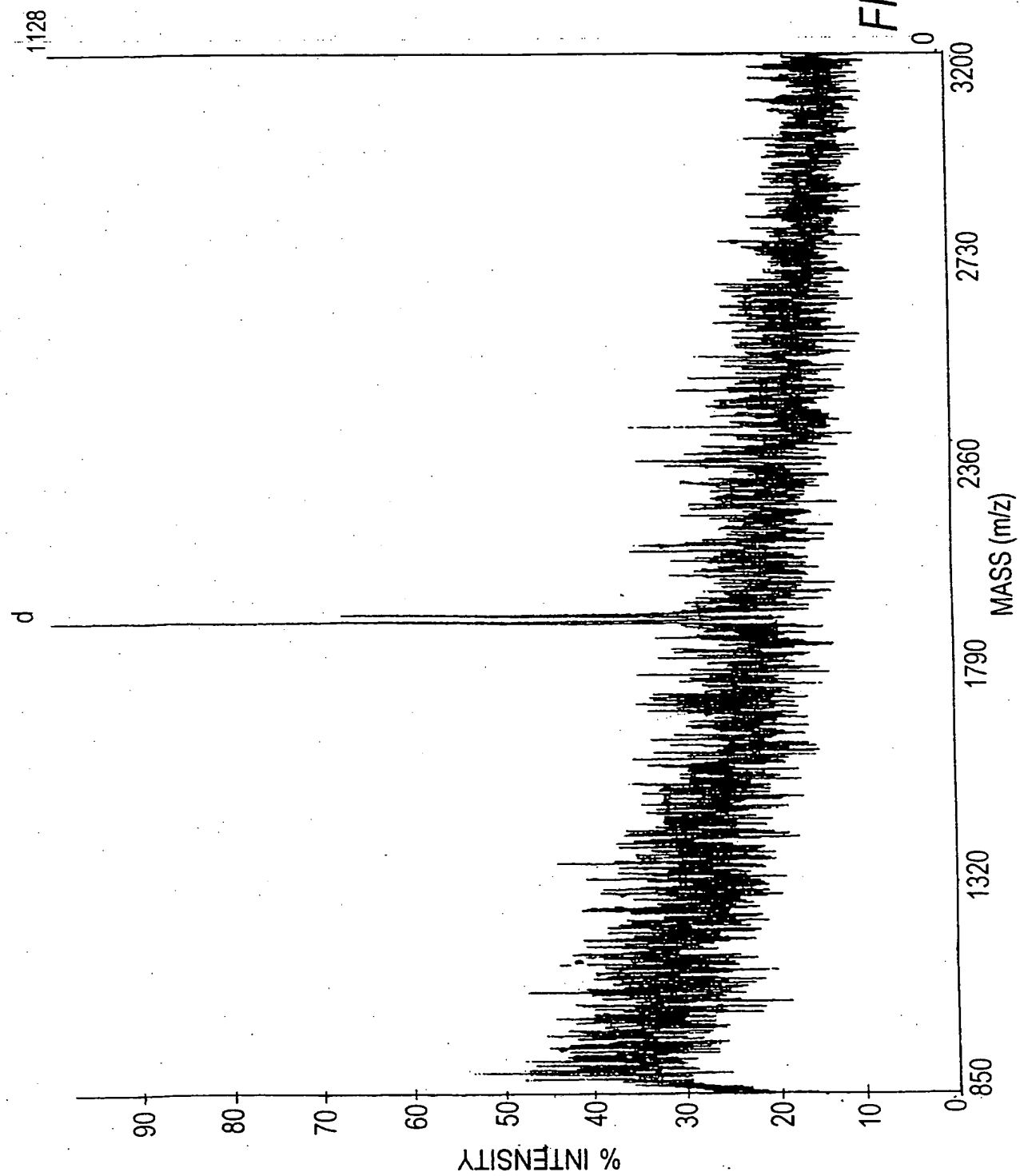
FIG. 12

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FIG. 12A

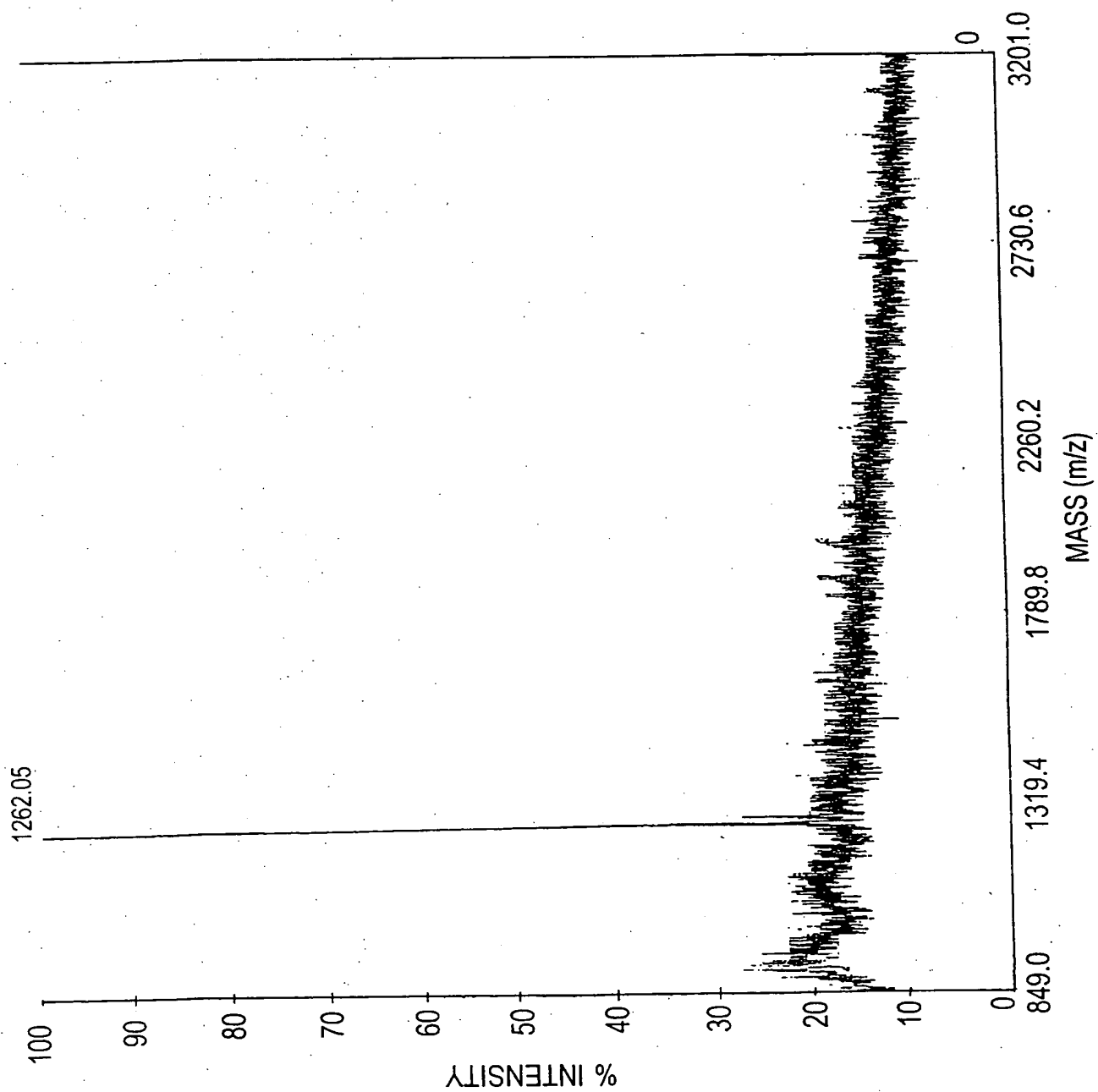


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FIG. 12C



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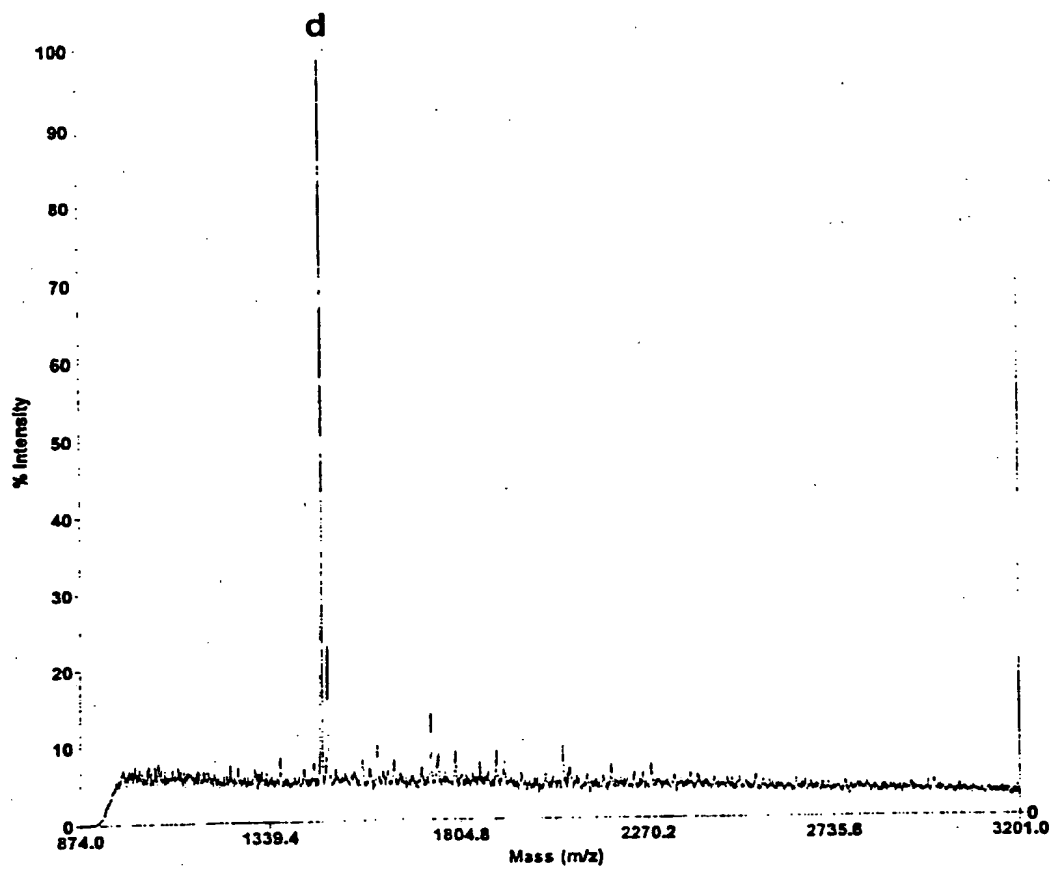


FIG. 13

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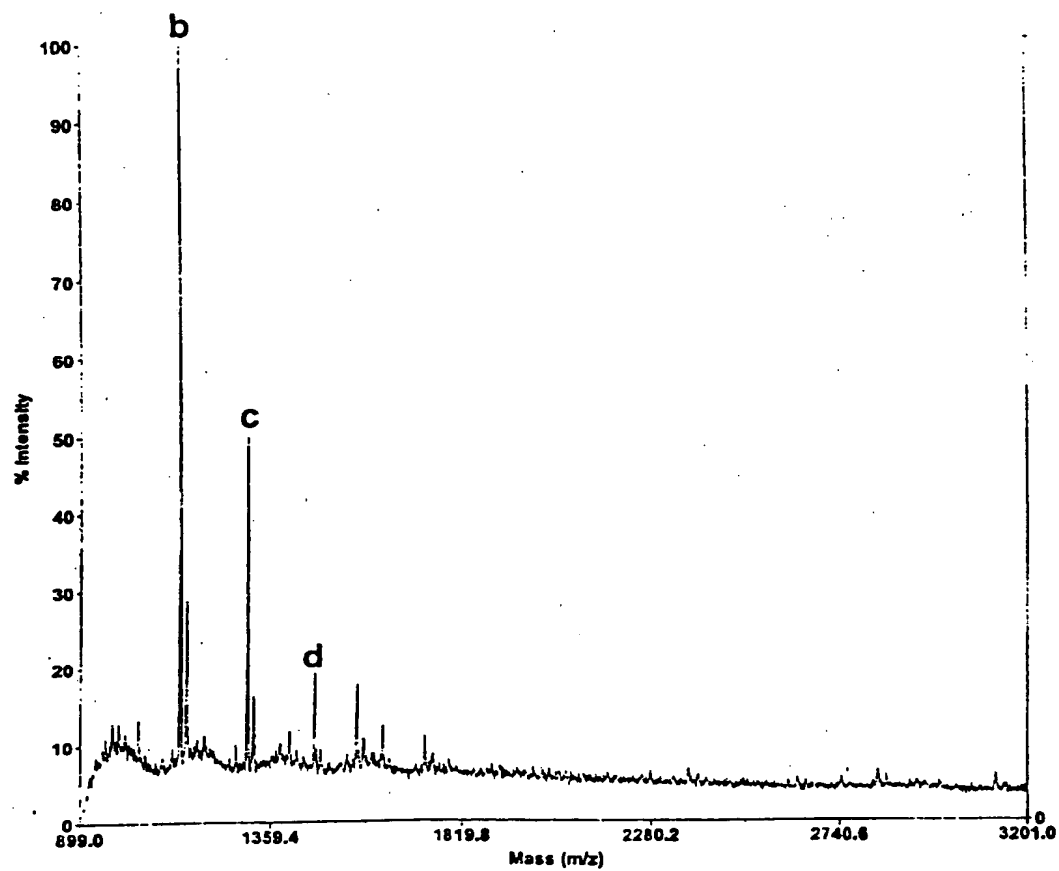


FIG. 14

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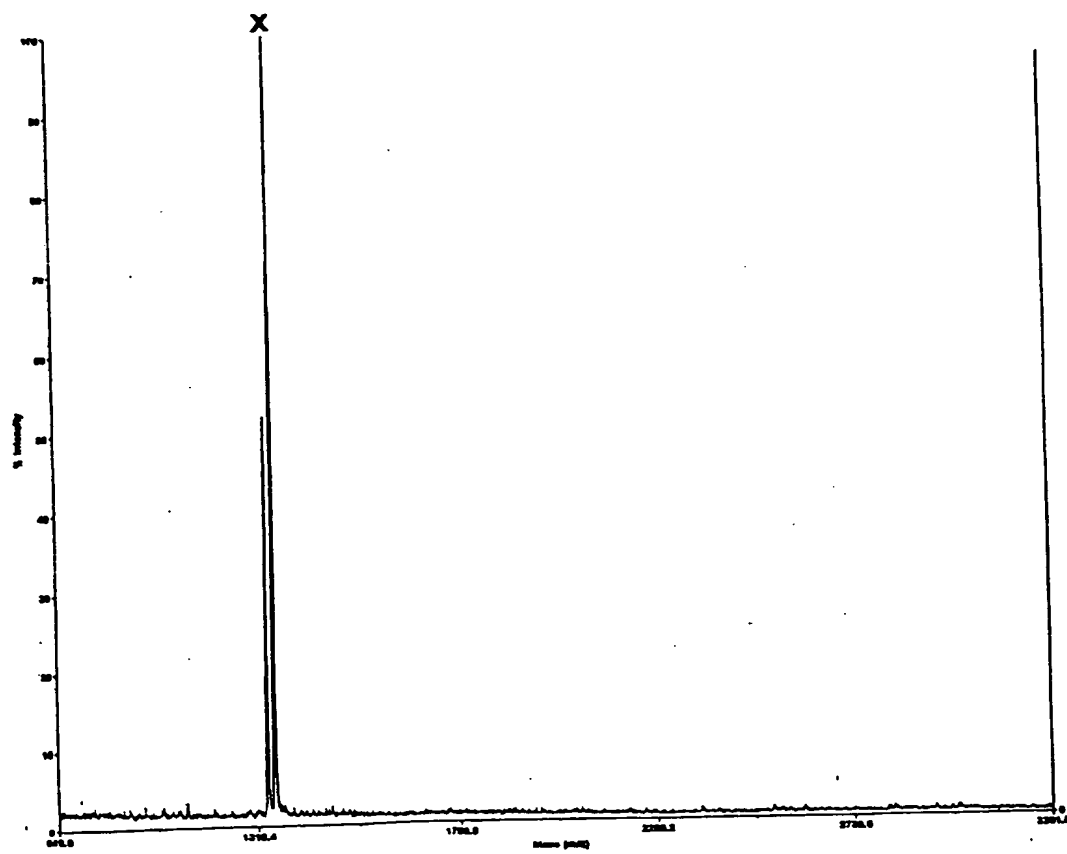


FIG. 15

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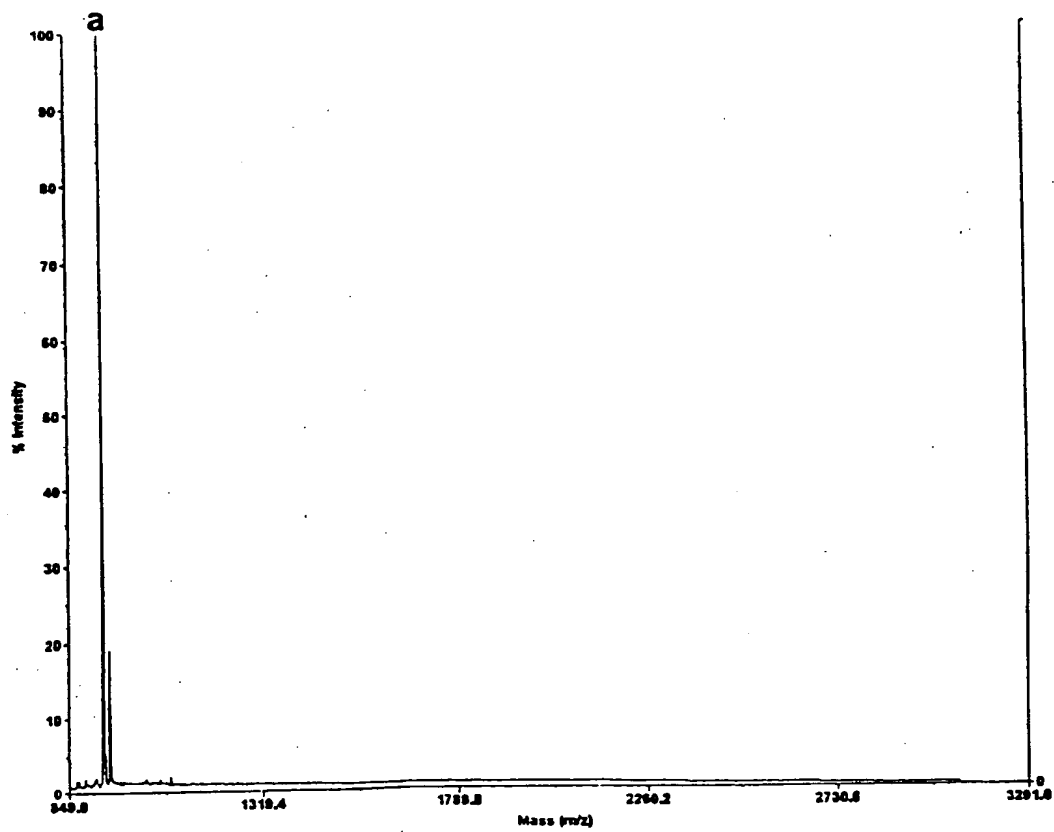
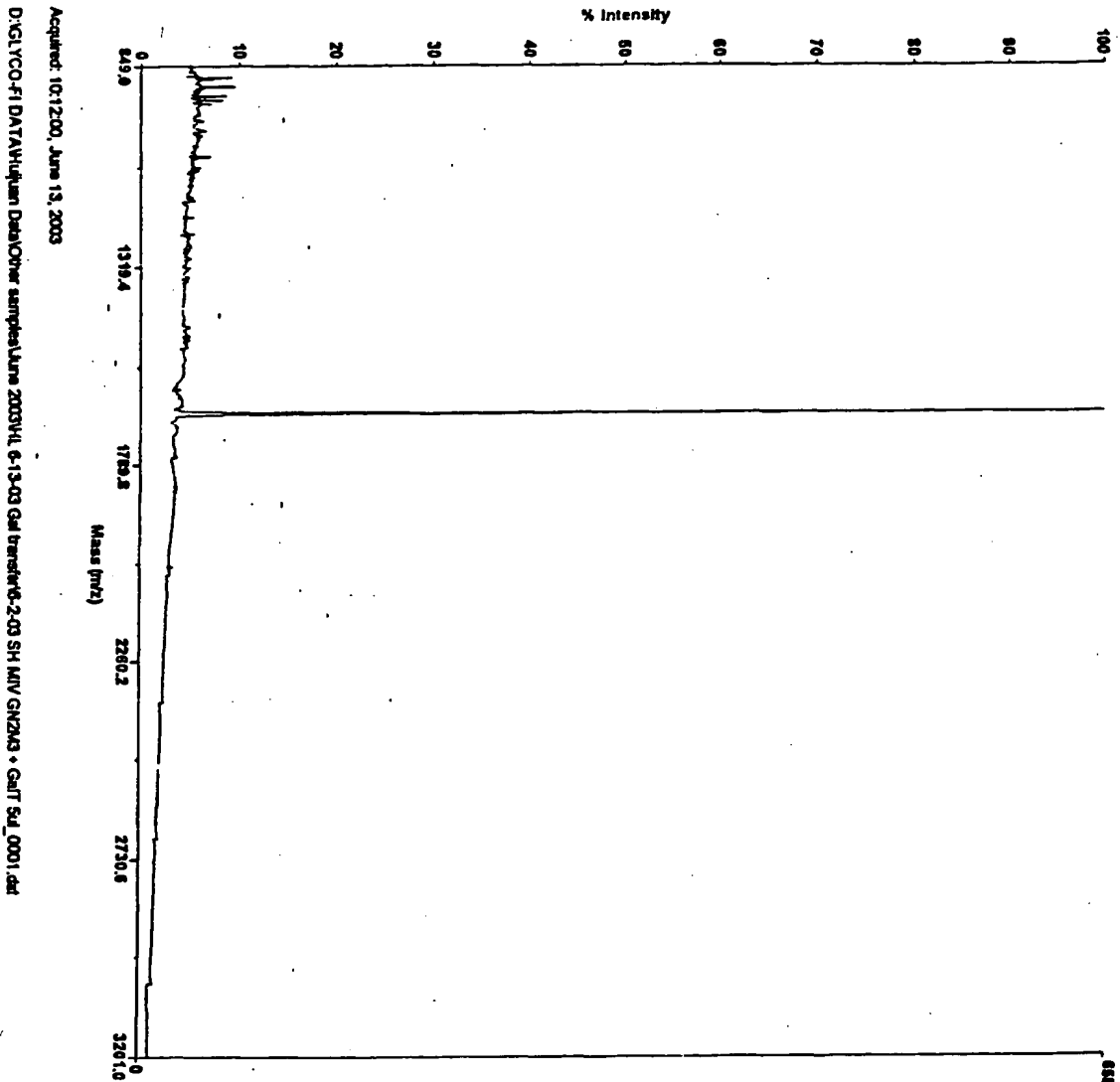


FIG. 16

Applied Biosystems Voyager System 1246

V. yager Spec #1246BC=NR(2.00)BP = 1664.6, 639]

FIG. 17



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual

Accelerating voltage: 20000 V
Grid voltage: 84%
Guide wire Q: 0.05%
Extraction delay time: 100 msec

Acquisition mass range: 850 - 3200 Da
Number of laser shots: 1000/spectrum
Laser intensity: 2713
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration method: 2,5-Dihydroxyphenolic acid
Low mass gate: 800 Da

Digitizer start time: 18.582
Bin size: 2 msec
Number of data points: 8676
Vertical scale: 500 mV
Vertical offset: 0%
Input bandwidth: 150 MHz

Sample well: 47
Plate ID: 100 WELL PLATE
Serial number: 1246
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.pl
Lab name: PE Biosystems

Absolute x-position: 31305.6
Absolute y-position: 28069.3
Relative x-position: -761.813
Relative y-position: 1081.83
Spots in spectrum: 100
Source pressure: 4.38e-007
Mirror pressure: 0
TC2 pressure: 0.00453
TIS gate width: 30
TIS flight length: 940

Printed: 08:41, June 16, 2003

Milestone IV Gal

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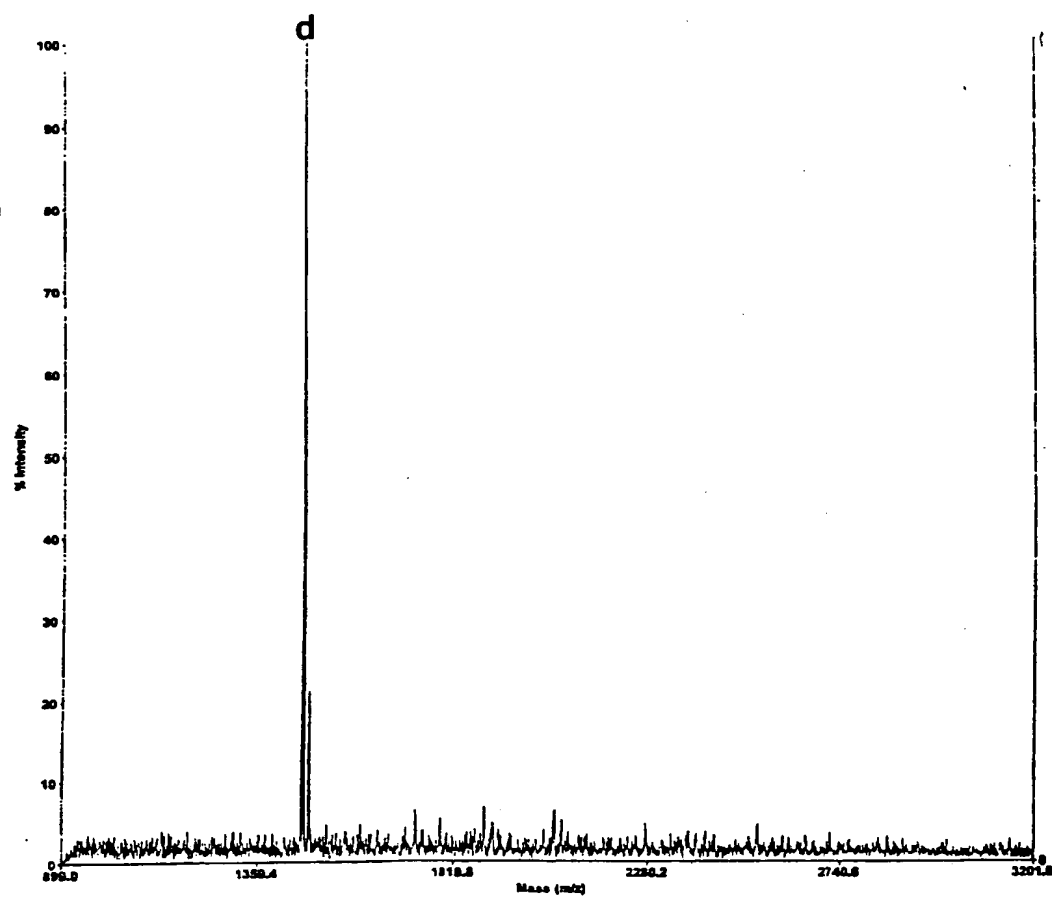


FIG. 18

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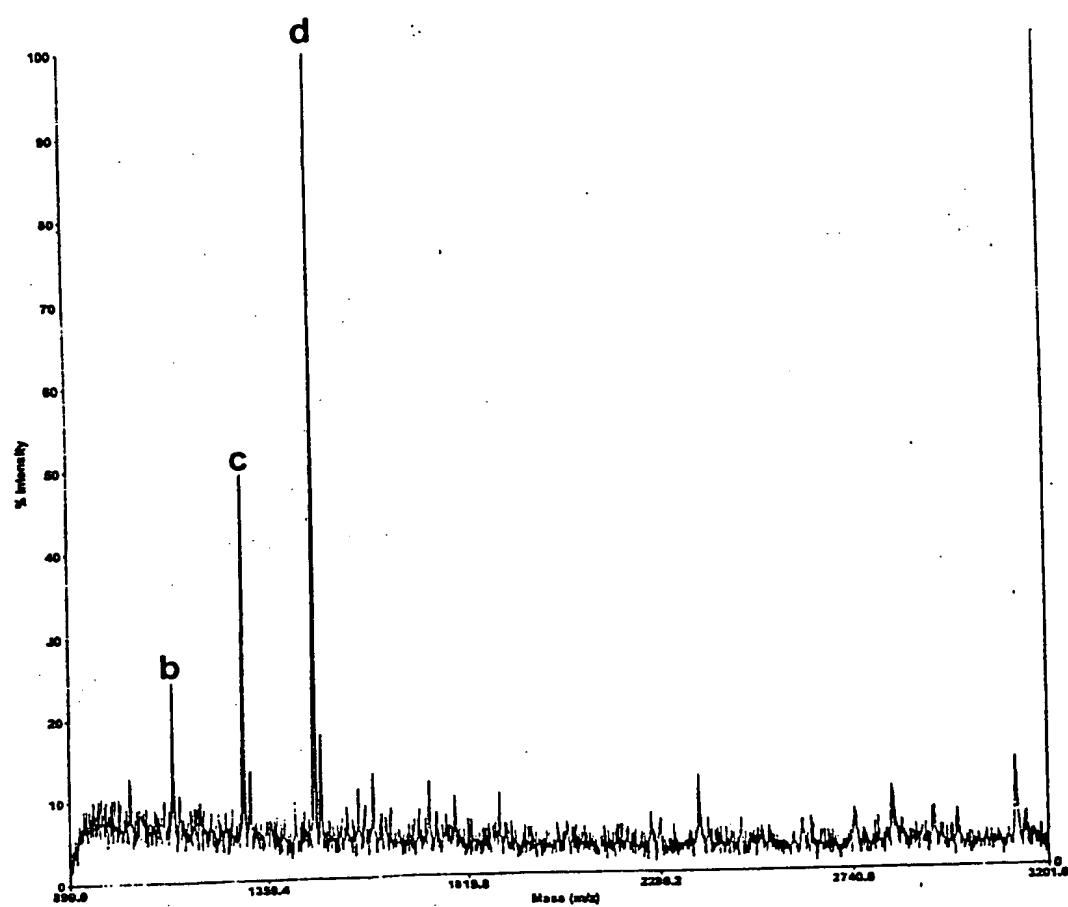


FIG. 19

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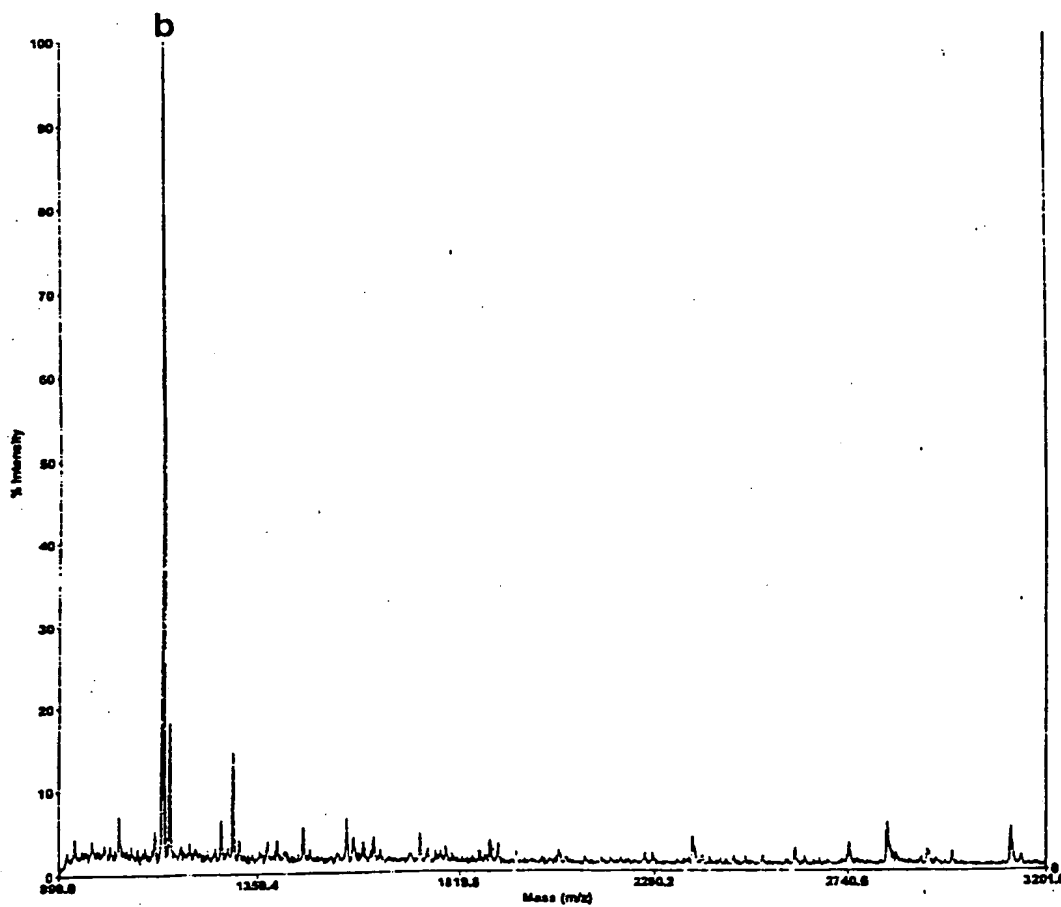


FIG. 20

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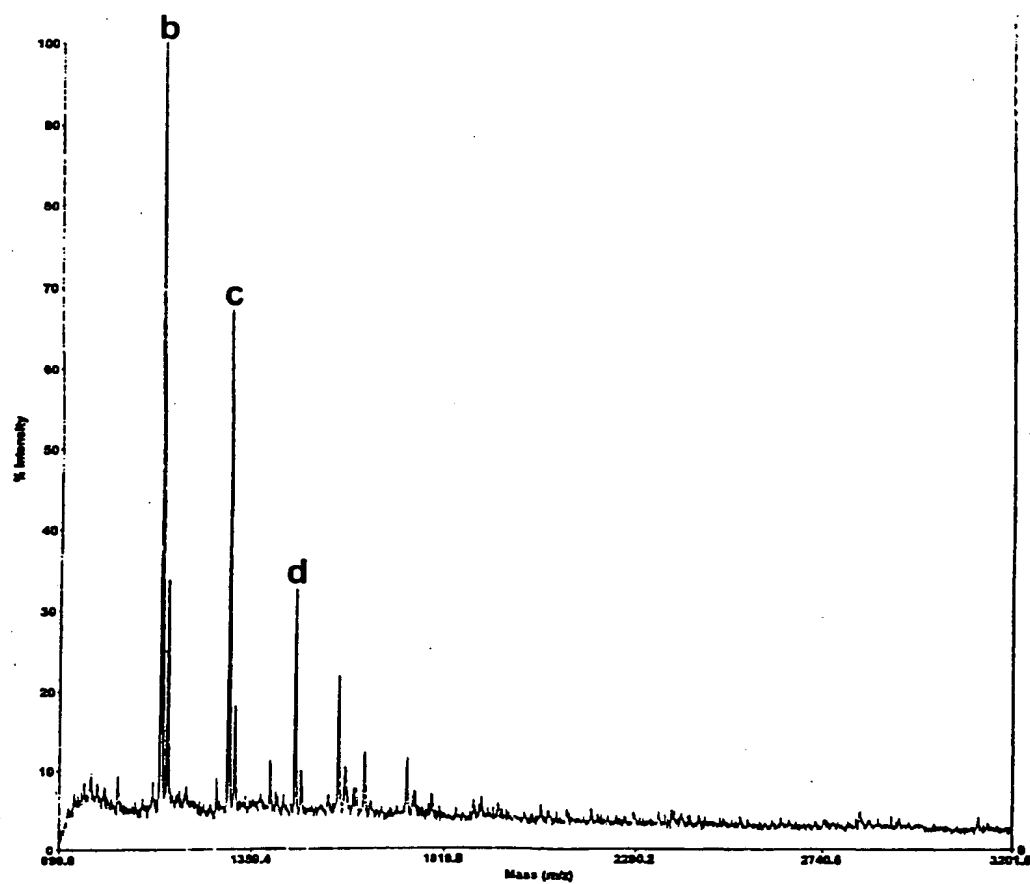


FIG. 21

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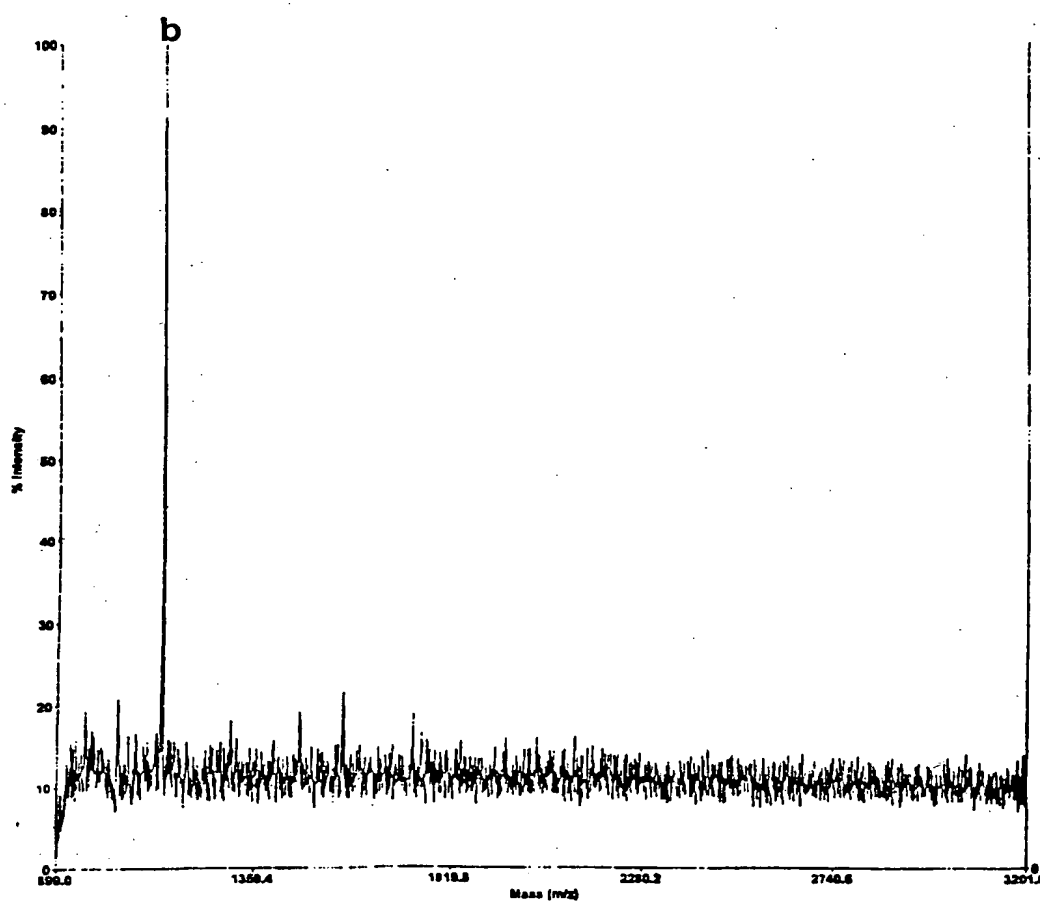
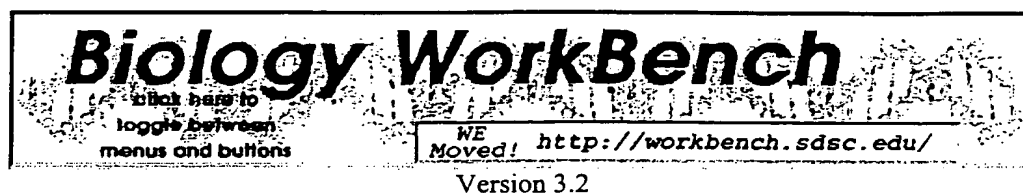


FIG. 22



BOXSHADE
Color-Coded Plots of Pre-Aligned Sequences

Selected Sequence(s)

- Drosu MannII (X77652),
C.elegans MannII,
rMannII (XM_218816.1),
hMannIIx D55649,
Mouse MannII (X61172),
human MannII (U31520),
CionaMannII (AK116684),
ArabMannII,
Insect ManIII,
hLyso MannII,
hCyto MannII (NM_006715)

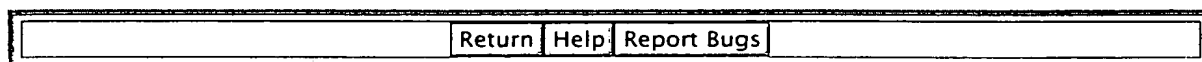


FIG. 23

Download a PostScript version of the output

```

Droso_MannII_[X] 1 -----
C.elegans_MannI 1 -----
rMannII_[XM_218 1 MACIGGAQGGQRAVEKEPSSHQGYPMWPMTHGSCSELALLSSTRMYCHQGCVRPPPTDVKN
hMannIIx_D55649 1 -----
Mouse_MannII_[X 1 -----
hMannII 1 -----
CionaMannII_[AR 1 -----
ArabMannII 1 -----
Insect_ManIII 1 -----
hLyso_MannII 1 -----
hCyto_MannII_[N 1 -----

Droso_MannII_[X 1 -----MRRRAA VICSGLVPLISLYIMFAAP-----AATQIRP
C.elegans_MannI 1 -----MGRFVY ILCIG-VPLTVSLTYXGIETG-----AEALTKR
rMannII_[XM_218 61 PRTTDTQSVPGVSYKRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS
hMannIIx_D55649 1 -----KRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS
Mouse_MannII_[X 1 -----KRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS
hMannII 1 -----KRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS
CionaMannII_[AR 1 -----KRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS
ArabMannII 1 -----KRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS
Insect_ManIII 1 -----KRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS
hLyso_MannII 1 -----KRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS
hCyto_MannII_[N 1 -----KRGVTCGAAIECAATSLITMDRVOHDPAR-HQNGGNFPRS

Droso_MannII_[X 40 YEMENRAREENGHQOEHGEERNAARARTNRD-----
C.elegans_MannI 37 CAMDARRRGMAEVAEENGRTDRHQEQRARAERSVDFDEERERTEEREVEKEERK
rMannII_[XM_218 120 SVLGNRECECLQEERREESHDSLEANAEGPALLPY-----
hMannIIx_D55649 46 SVLGNRECECLQEERREESHDSLEANAEGPALLPY-----
Mouse_MannII_[X 47 SVLGNRECECLQEERREESHDSLEANAEGPALLPY-----
hMannII 47 SVLGNRECECLQEERREESHDSLEANAEGPALLPY-----
CionaMannII_[AR 45 SVLGNRECECLQEERREESHDSLEANAEGPALLPY-----
ArabMannII 37 SVLGNRECECLQEERREESHDSLEANAEGPALLPY-----
Insect_ManIII 28 YCYFYASPOHYNPRISYPASREYSSSTETVK-----
hLyso_MannII 1 YCYFYASPOHYNPRISYPASREYSSSTETVK-----
hCyto_MannII_[N 34 RFGASCPAVVSSPPTPERLPYQAVQDPRPAQVG-----

Droso_MannII_[X 77 -----DPIRPPLVARSPRPGCCQDVQDVPHVDOMTEMDRSEPDID
C.elegans_MannI 97 APVPVRGNRGMABIRQVQRIKPTPSMDVCGIRENVSIABSDOMIDRDTWKEPNPD
rMannII_[XM_218 166 -----HTANGSMVLPPEPRSPFSVSPEDCPALGGRGQRPOMITSEEDPPEINV
hMannIIx_D55649 92 -----YTVNGSMVLPPEPRSPFSVSPEDCPALGGRGQRPOMITSEEDPPEINV
Mouse_MannII_[X 93 -----NASQGS-IELSPOLA-LQADPRDLFASQSGSQPRNDOMIDYDLPEPNPD
hMannII 93 -----NFSQGAGSRLPLPSQLS-LSVDTADLFASQSGSHNSDOMIDYDLPEPNPD
CionaMannII_[AR 94 -----NFMKPVLPPLIMPCQFANDSRMDTCPVLSYGGKSDOMIDYDLPEPNPD
ArabMannII 83 -----SRPLTSRSNRIVPRRNINRRPLINDSNAGAVVITRDYDLPEPNPD
Insect_ManIII 63 -----SDEPTDQCPALKEHADIDTAYPTDQPSMLRT
hLyso_MannII 13 -----GCLDSAGPMTMSRALEPPLPPCFPLLIQAAGAR
hCyto_MannII_[N 71 -----DSFGPTWNTCMFRVELTIPAMGQEVLCWESDG

Droso_MannII_[X 122 GGVWROGRIEPLRMAHRRFAVVPVPHSHNDPG-----CT
C.elegans_MannI 157 GGVWROGRIEPLRMAHRRFAVVPVPHSHNDPG-----MT
rMannII_[XM_218 219 GGVWROGRIEPLRMAHRRFAVVPVPHSHNDPG-----RT
hMannIIx_D55649 145 GGVWROGRIEPLRMAHRRFAVVPVPHSHNDPG-----RT
Mouse_MannII_[X 144 GGVWROGRIEPLRMAHRRFAVVPVPHSHNDPG-----RT
hMannII 145 GGVWROGRIEPLRMAHRRFAVVPVPHSHNDPG-----RT
CionaMannII_[AR 147 GGVWROGRIEPLRMAHRRFAVVPVPHSHNDPG-----RT
ArabMannII 132 GGVWROGRIEPLRMAHRRFAVVPVPHSHNDPG-----RT
Insect_ManIII 101 KEFQKSKDRIRHNTTRPRFAVVPVPHSHNDPG-----RT
hLyso_MannII 48 AGGETCPTOPHMAVVPVPHSHNDPG-----RT
hCyto_MannII_[N 107 GIVWDGEPGLTKGRTS-YLTDRLGERDERS-----ITLY

Droso_MannII_[X 162 EERYQ-----HDTRHITSWARRHTEEMFIABISFAAHDGEYRLO
C.elegans_MannI 197 EERYQ-----ROTNRIDGAREJA KDEMFIABISFEETMRDOADEIKKV
rMannII_[XM_218 277 EERYQ-----EOTCRILNVSRLCEDPRRFAEVSFAAHDGEYRLO
hMannIIx_D55649 184 EERYQ-----EOTCRILNVSRLCEDPRRFAEVSFAAHDGEYRLO
Mouse_MannII_[X 183 EENDYR-----DTCYFPMVLEIKDSSRFI SEISLAHNDIDIRBAV
hMannII 184 EENDYR-----DTCYFPMVLEIKDSSRFI SEISLAHNDIDIRBAV
CionaMannII_[AR 186 EERYQ-----DTCYFPMVLEIKDSSRFI SEISLAHNDIDIRBAV
ArabMannII 171 EERYQ-----ROTNRIDGAREJA KDEMFIABISFEETMRDOADEIKKV
Insect_ManIII 142 EERYQ-----EOTCRILNVSRLCEDPRRFAEVSFAAHDGEYRLO
hLyso_MannII 80 VQYLYGIRNDIQBAGVCIYDSASALLADETRFIVEIAFESMBOOTMATQEVV
hCyto_MannII_[N 146 VEYACN-----GLLGAGRGSAAPDPTRIPQLSRFAVERDVHM LVDIELLG

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rMannII_XM_218 715 GSQST HPSAALVPAALASA LPQR-AP PVV MPL CRRLS V IVNSPR RV SEE
 hMannII_D55649 630 LSADA P-----ERTV QLDS-SP PVV MPL CRRLS V IVNSPR RV SEE
 Mouse_MannII_X 629 SSQDS P-----QRIT QLSAQEP Y V MPL CRRLS V RVNSATGV SDS
 hMannII 630 SSQDS P-----QRNI RLSE-EP Y V MPL CRRLS V IVNSPT QVSAS
 CionaMannII_[AR 626 QHQOPAP-----VVVR PTNEERAVV QMSL YDRIS V IVNSPD VVSRN
 ArabMannII 627 YDARP HRP-----AAREGNSETV MPS OTREE V VVNRAS SV DSN
 Insect_ManIII 590 PRK-----QVSPIDR V MPLAETRE V RSN SN RYDTH
 hLyso_MannII 508 R-----FQV MPLGRVNV V PSEGVV VVDPN
 hCyto_MannII_[N 583 -----SCIQVAREZAE ED RSRGNT AAAAAALCAGEPGPE

Droso_MannII_[X 648 N-NPVEAO SPVW WRRDTLTKTIRPOGSTK R IFKAR EP GHATV TIS-DSRPE
 C.elegans_MannI 674 P-PIKKCO SPVIAYDEERTLVVNG-----I CFML GP ESVS R VKN-TTTSK
 rMannII_XM_218 774 C-OP SVO SVOM SATMVDP-----V C SVPRV PALGIGVLC OPDLDGPT
 hMannII_D55649 680 C-OP LAVO SAHM SATRAVPD-----V C SVPRV PALGIGVLC QLGIDGHT
 Mouse_MannII_[X 680 C-KPVEVO SAV NDMRTISQA-----A SFLAR PPLGIRV R LESQSSSSH
 hMannII 680 C-KPVEVO SAV DTANTISRT-----A SFLAR PPLGIRV R LESQSSSSH
 CionaMannII_[AR 677 K-NVPSQTSPI DSTRITD-----C VELS PA GLAVYR WEDNDVADT
 ArabMannII 676 W-TCVPSO SPEVCHDDTLFTG-----EBR Y RA PALGIRV R ANGEVCEK
 Insect_ManIII 633 RREBVLYO MDSI IQDNCKSIVS-----DTT MFVA PPTTSISYR QERTTSHR
 hLyso_MannII 541 C-RTVPSD VIPP SDSQAHPP-----ELFA PALGPTSL AQVPRWKPQ
 hCyto_MannII_[N 623 C-L IV TLFWRRIEVMALPRPG-----GARSLAV ES CTAPVPPPTSLQPLP

Droso_MannII_[X 706 HTSYASHLLLRNPTSLPIGC PED KFGDPR RVGNGLTAPSE---QGLL S QL
 C.elegans_MannI 728 VEITTHNAAEPRTSFSSSTSGDPT RNDRV AEP GENGM KRATS---LVDD P DL
 rMannII_XM_218 824 LQSSVHYLNGVLSVSRQTT P R DSGTS FA SMRY C MSLG---TGLL S RR
 hMannII_D55649 730 LPSSVRYLNGVLSVSRRA P R DSGTS FA SMRY C MSLG---TGLL S RR
 Mouse_MannII_[X 730 LADYVLYND-----GLAEMGI H N VADGA CMPP A M D-R---GLI ER RR
 hMannII 730 LADYVLYR-----EVDSGI T M INTREG ANSP L M D-Q---GLI ER RR
 CionaMannII_[AR 727 TRSTVVKP INPRVGSRTSRK V D EDSG---F M MDO VAPSSGO---NGS QS TT
 ArabMannII 727 ATPSKLYASEPDPFPCPP-----PYSCSKLDNDVTE RNEHOT VEDVR---NGSL R VR
 Insect_ManIII 688 CVIPCNH-----CQYQKSNVFO KMMPG TO ENAV RLVNR---TGFL R YR
 hLyso_MannII 589 ARAPQP-----IPRRSWSPA ENER RATDPD---TGILX MN
 hCyto_MannII_[N 674 QQ-----PFP VQETDGS ENGI R KIDPTGRLTSL LVASG

Droso_MannII_[X 763 TC SPHPVPVPRFLK VRSBGDS---GAYLELPMGPASVEVLCQ---V
 C.elegans_MannI 785 NSPFIHYGARRSKR ANGEDHPA---GAYLELPDGARELRQSS---D
 rMannII_XM_218 881 V EHQEQVD KLFV RTSDS---GAYLELPDN AREVPRKE---PV
 hMannII_D55649 787 V EHQEQVD QLVK RTSDS---GAYLELPDG ASPTSPSE---PC
 Mouse_MannII_[X 782 R EHQEQVD QLVK RTSDS---GAYLELPDG COPTVSLR---PF
 hMannII 781 R EHQEQVD QLVK RTSDS---GAYLELPDG AREVPRKE---PF
 CionaMannII_[AR 782 V EHQEQVD QLVK RTSDS---GAYLELPDG AREVPRKE---PF
 ArabMannII 781 R EHQEQVD QLVK RTSDS---GAYLELPDG AREVPRKE---PF
 Insect_ManIII 738 R EHQEQVD QLVK RTSDS---GAYLELPDG AREVPRKE---PF
 hLyso_MannII 628 MHOQLLLP VQTPFV MASIGDNESDQAS GAYLELPMGPASVEVLCQ---I
 hCyto_MannII_[N 714 R EHQEQVD QLVK RTSDS---GAYLELPDG AREVPRKE---PF

Droso_MannII_[X 808 ILVRSK ESSVSG-----LPS VROT---IMRGS-----AP RNLVD G-S-LDNT
 C.elegans_MannI 830 WLVRSK VORVPATPHDLKI OTMT---LYOGL---PM DNEVD R-S-KMP
 rMannII_XM_218 927 RLVRSK PPFSEUAA YEPHOV MLYN---LPGVEG-----LS SFOVD R-D-YVM
 hMannII_D55649 833 C-----VSLKALSQRMLRT IST T-RR-SG---FT CQGWRCG---T-YHPW
 Mouse_MannII_[X 828 RLVRSK YSDVTC LEBVTR RLYN---IQGIES---QS SNIVR R-W-VN
 hMannII 827 RLVRSK YSEVTC PDBVTR RLYN---IQGIES---QS SNIVR R-K-YVM
 CionaMannII_[AR 829 RLVRSK YSDVTC LEBVTR RLYN---IQGIES---QS SNIVR R-W-VN
 ArabMannII 821 VTESLVQEVF SPRTMERSPLS ORTRLYTGTTLQOV AREVPRKE LG-WDFDD
 Insect_ManIII 792 ILVRSK PPFSEUAA YEPHOV MLYN---LPGVEG-----LS SFOVD R-D-YVM
 hLyso_MannII 678 RLVRSK YSDVTC LEBVTR RLYN---IQGIES---QS SNIVR R-W-VN
 hCyto_MannII_[N 759 RLVRSK YSDVTC LEBVTR RLYN---IQGIES---QS SNIVR R-W-VN

Droso_MannII_[X 852 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 C.elegans_MannI 879 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 rMannII_XM_218 977 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 hMannII_D55649 874 WTSG---TTSTSNWPC---TSIOTSTAR OPRY-----DRILPQAN YP PGM E
 Mouse_MannII_[X 878 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 hMannII 877 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 CionaMannII_[AR 882 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 ArabMannII 880 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 Insect_ManIII 846 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 hLyso_MannII 727 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 hCyto_MannII_[N 814 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E

Droso_MannII_[X 902 DAX---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 C.elegans_MannI 929 DDT---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 rMannII_XM_218 1027 DSO---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 hMannII_D55649 922 DAX---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 Mouse_MannII_[X 928 DAX---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 hMannII 927 DAX---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 CionaMannII_[AR 932 DEX---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 ArabMannII 930 GSG-ORF VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 Insect_ManIII 898 DEX---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 hLyso_MannII 785 DEX---TRITLITAC LGSSSIASGELE DERRIASDDERGLGCGVNDNRPLVRI R
 hCyto_MannII_[N 858 LSEHGFGTADNDCKYAS---VRGS LS SLRAPRAPDATATERR PLYALMPH GSF

Droso_MannII_[X 960 E VRSK ETR DSGDI---PYTDLNGLOP IRR-----DRILPQAN YP PGM E
 C.elegans_MannI 987 EPM SSSGNKREE-----RVG RSH GRASVIRYP K IGDA
 rMannII_XM_218 1085 E R L SPEVQOR-----RSTSPSL SH TSMYLNTPP V P AR
 hMannII_D55649 980 E R VGS RVQDS-----RSTSPSL SH TSMYLNTPP V P AR

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Mouse_MannII_[X 986 E R A NMEERER-----SPVSYPSTLSE TSSFLRPP P V SG
hMannII 985 E R A NTEERER-----S-VSYPSTLSE TSSFLRPP P AN--
CionaMannII_[AR 990 E M A AAREERSS-----AKLAKPSRAVYQSSWELEP RP S NG
ArabMannII 989 ESNISQADPASNT-----NPRNPSLSE IGARLPP NTFLAKK
Insect_MannIII 956 ESMQPG TRAKRDTSEPGFYPVNERRPFGPGQKESPYQVPSOTADYISRMPTP NVYI DT
hlyso_MannII 843 VLLDTAQAAAAGHR-----LAEQELAEQV LAPGG
hCyto_MannII_[N 916 QDAGV CAAYSLN-----ELIALPAPSPAPATSMWAFS SS

Droso_MannII_[X 1000 NEWIGAQGO-----FGGDEESAREDD SV RRLTKS-----
C.elegans_MannI 1027 TPESISSKN-----EORFPCD BL TPR ASPTTY-----
rMannII_[XM_218 1126 RESTSPT E---SEPTIASP LFCDFELLMLRM PAEVSVPVRANPHERQAEPCLLGRRAAD
hMannIIx_D55649 1020 MQLPGPG R---SEPTIASP LFCDFELLMLR QAE-----
Mouse_MannII_[X 1027 -QLPSPAYELLSEFP LQSSLP CD BL MLR QSKMG-----
hMannII 1023 -KFSPT ELQGEFSP LQSSLP CD BL MLR QSKVG-----
CionaMannII_[AR 1032 -----P ELRED RSIPQ LFCDFELLMLRA BSKDA-----
ArabMannII 1029 PDISVR PQYGSFAP LARPLCD BL MF VPRPSKYS-----
Insect_MannIII 1016 SEVGRIE RP---QSFLOSFP PG BL TLR TDDVLE-----
hlyso_MannII 875 GAAYNLGAPPRTQPSGPRDLPS BLITLA WGPBMVLR-----
hCyto_MannII_[N 953 PAVVLET R---QAESPPQRSLVRLYEAH-----

Droso_MannII_[X 1032 -----SARTQVY Y HRTFLMCC TPEERTQKLDVCHLLPFWARCERTT TFL
C.elegans_MannI 1059 -----EAMERST YERKAAMVMHRV PDCR-SRLTLPTDSCLATGLEIEP RI
rMannII_[XM_218 1183 PPPLLSLTVPQDTLPAAD YP LEREG YC SEAH GPNC T OGRVAIGSLPHG D L
hMannIIx_D55649 1054 -----DTLP ARTAL LEREG YC SEAH GPNC T OGRVAIGSLPHG D V
Mouse_MannII_[X 1064 -----RGY DE AL LEREG YC OFSS G GLPC T OGRMSVLKLPNKA E
hMannII 1060 -----MGR NE AL LEREG YC OFSS GTGLFC T OGRILVQILLNKP I E
CionaMannII_[AR 1064 -----VAP DQSAL LEREG YC DADRYFPTCLMEGVERLAITIST PTH
ArabMannII 1068 -----QLEEDKPRPAL LEREG YC YCEGRQVNC SMANEPVHFSDMPKDLAA
Insect_MannIII 1052 -----LPP NESY LEREG YC SCAGE P AKSPKP SKTRFNLNIQW TAV
hlyso_MannII 916 -----LEHOFVAVEDSGRLSAPVT NLD PSTP I RLQETTLVANQLREAA
hCyto_MannII_[N 981 -----G RVDC YRLSLPVQE LCDL ERPDPAHLTSGQPPFAHLFS P

Droso_MannII_[X 1081 QMPERLDGM APEVCPME-----TAAY SESS-----
C.elegans_MannI 1107 STPSARE S TNLYEGR-----KAEQRTQEM IS I SP-----
rMannII_[XM_218 1243 F-HQP STSL YPLASPS-----ESTD STPEMEIST RUG-----
hMannIIx_D55649 1103 F-HQP STSL YPLASPS-----ESTD YTEPMEIAT RUG-----
Mouse_MannII_[X 1112 S-HVP STSL RSPPDAQ-----NMSE STSPMEIST RUMWT-----
hMannII 1108 S-HTP STSL RSPPGTO-----NISE MISPMEIST QIR-----
CionaMannII_[AR 1112 SG RR STSL RDGSLLD-----NOGG STSPMEIOA VIT-----
ArabMannII 1119 SR RP STSL QEDMEILGYDDQLPRDSSQPREGR STSPMEIRA EIRPHK-----
Insect_MannIII 1100 SLTGLR STP TG-----LSD RIFAMEE RT RF-----
hlyso_MannII 965 SRPRW EY GPPTPHQTPY-----QLDPAN STPEMEIST LAS QWKEVDG
hCyto_MannII_[N 1027 SAPVARA LASATLSPWG-----WGFVCRDWG ILSASPA-----

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Citation

Algorithm Citation:

Not given, but presumably Kay Hofmann and Michael D. Baron.

Program Citation:

Boxshade version 3.3.1, by Kay Hofmann and Michael D. Baron.



FIG. 24

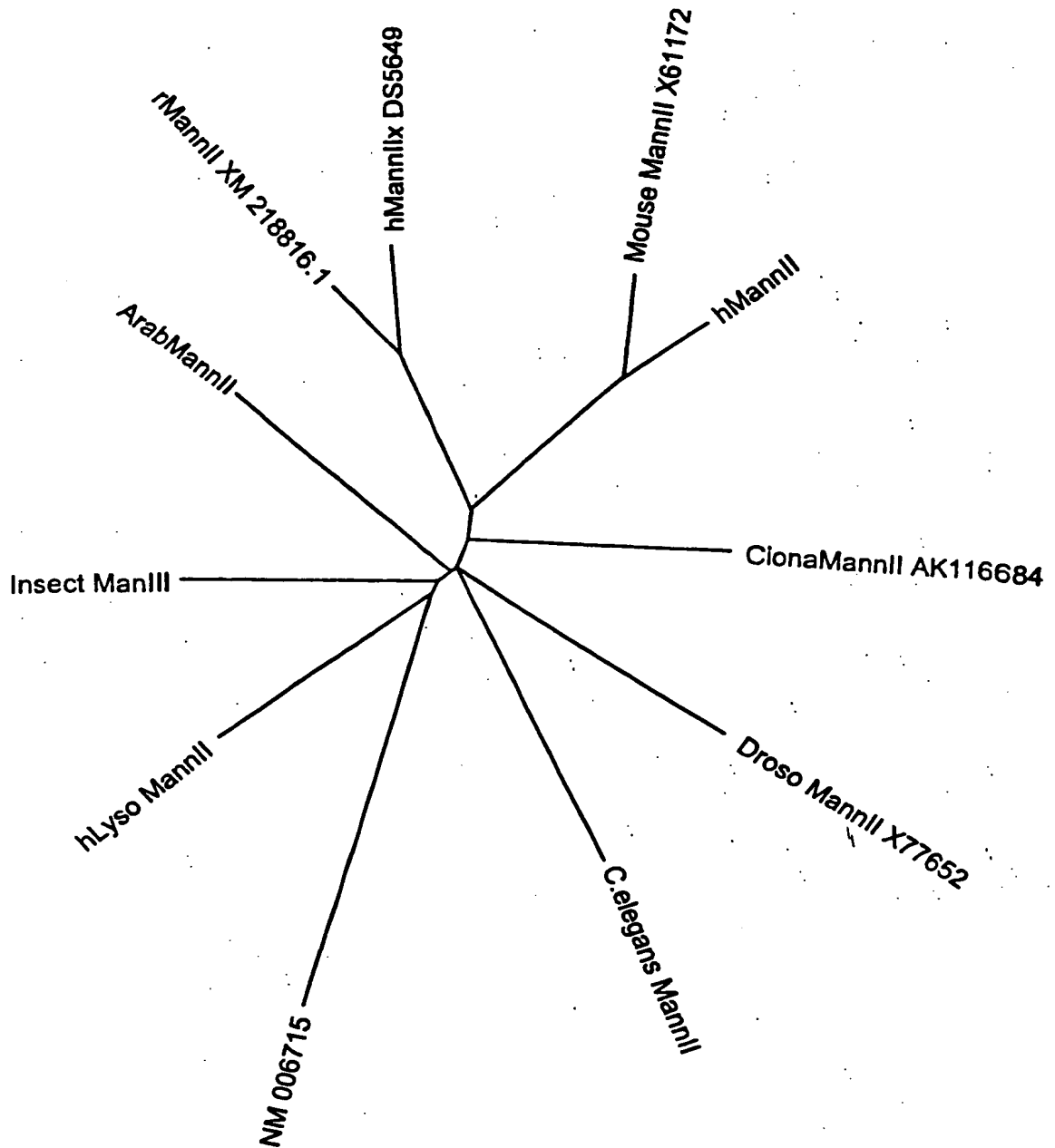


FIG. 25

Arabidopsis thaliana Mannosidase II (NM_121499)

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1  ATGCCGTTCTCCTCGTATATCGGCAACAGCCGCGTAGCTCCACCGGCGGAGGAACCGGCGTTGGGGCCAATCTTCTTCCAACAGCGTTATCAAAGTCAAACTAG
101 M P F S S Y I G N S R R S S T G G G T G G W G O S L L P T A L S K S K L
110 CGATCAATCGAAAACCGAAAACGAACTCTCGTAGICAAATTTTCATCTTCGCCAATCTTCTGTCATCGCACTCACCGTCTCACTCTCTTCTTCTCTCTCACTCTCTT
37 A I N R K P R K R T L V V N F I F A N F F V I A L T V S L L F F L L T L F
219 CCACCTTCGGCGTACCAGGACCGATCTCTCAGCATTCTTACCTCCAGATCCAATCGGATCGTCAAGCCACGGAAGAATATTAAATCGCCGACCTTAAACGATTCCAAT
73 H F G V P G P I S S R F L T S R S N R I V K P R K N I N R R P L N D S N
328 TCAGGCGCGCTCGTTGATATCACAATCAAGATCTATACGATAGGATGAGTTTCTTGATACAGATGGTGGTCCATGGAACAGAGTTGGAGAGTTACGTATAAAGACG
110 S G A V V D I T T K D L Y D R I E F L D T D G G P W K Q G W R V T Y K D
437 ATGAGTGGGAGAAAGAGAGCTCAAAATCTTCGTTGTTCTCTCATTCTCATAACGATCTCGTTGGAAATGCACTGTAGAGGAGTATTATCAGAGACAAATCCAGACATAT
146 D E W E K E K L K I F V V P H S H N D P G W K L T V E E Y Y Q R Q S R H I
546 TCTTGACACCATTTGTTGAGCTTTATCTAAGGATTCAAGAAAGAACTTTATATGGGAGGAGATGTCATATCTGGAGAGATGGTGGAGAGACGCTTACCTAATAAACA
182 L D T I V E T L S K D S R R K F I W E E M S Y L E R W W R D A S P N K Q
655 GAAGCTTTGACTAAATTTGGTTAAGGATGGGCGCTAGAGATTGTTGGAGTGGTGGTTATGAATGATGAGGCTAATTCACATTATTTGGCCATAATTGAACAGATAG
219 E A L T K L V K D G Q L E I V G G G W V M N D E A N S H Y F A I I E Q I
764 CAGAGGTAATATGTGGTGAATGACACAATTTGGGTTATTCTTAAGAATTTCTGGGCTATAGATCCCTTTGGCTATTTCATCAACCATCGCTTATCTTCTCGGCGTAT
255 A E G N M W L N D T I G V I P K N S W A I D P F G Y S S T M A Y L L R M
873 GGGTTTGAAGACCTGCTTATCAAGGACTCATTACGAGCTCAAGAAAGACCTTGGCCAGCATAAGAATCTTGAATATATTGGCGTCAGAGCTGGGATGCTATGGAA
291 G F E N M L I O R T H Y E L K K D L E F L D T D G G P W K Q G W R V T Y K D
982 ACCACAGATATCTTGTTCATATGATCGCGCTTTATTTCATACGATATCCACACACTTGTGAGCAGAGCGCTGCAATTTGCTGTGAGTTGCAITTCGCTCGGATCGGG
328 T T T D I F V H M M P F Y S Y D I P H T C G P E P A I C C Q F D F A R M R
1091 GATTTAAGTAACTTTGTCATGGGGAAGCACCAGTGGAGACCACTAGAAAATGTGCGAGGAGGGGCAATTAAGCTTCTGGATCAATACAGGAAAAATCCAC
364 G F K Y E L C P W G K H P V E T T L E N V Q E R A L K L L D Q Y R K K S T
1200 TGTATATCGAATAATACACTTCTTATACCTCTTGGAGATGATTTTAGGTACATTAGTATCGATGAAGCCGAGGCTCAGTTCCGTAACCTACCAGATGTTGTTTGTATC
400 L Y R T N T L L I P L G D D F R Y I S I D E A E A Q F R N Y Q M L F D H
1309 ATCAACTCTAATCTAGTCTAAACCGCAGAACAAAGTTGGTACTTTGGAGGATTTTTCAGAACAGTCCGAGAAGAACGACAGAGTCAATTTCTCGTCTCGTG
437 I N S N P S L N A E A K F G T L E D Y F R T V R E E A D R V N Y S R P G
1418 AGGTGGCTCTGGTCAGGTGTTGGTTTCCCTTCTCTGTGAGTGACTTCTTACATATGAGATAGGCAACAGACTATTGGAGTGGTTATTTATGTTTCAAGACCTTT
473 E V G S G Q V V G F P S L S G D F T T Y A D R Q Q D Y W S G Y V S R P F
1527 CTTCAAAGCTGTTGATCGTGTGCTCGAGCATACCTTCTGTGAGCTGAGATCATGATGCTATTCTGCTAGGTTATTGGCATCGAATCAATGTCAGAAATTTCAACA
509 F K A V D R V L E H T L R G A E I M S F L L G Y C H R I Q C E K F P T
1636 AGTTTTCATATGAATTTGCTGCTGCAAGAAGAAATCTGGCTTTTCCAGCACCATTGAGGGTAACTGGAAGTCTGTAAGGATTTGCTGCTACAAGATTACGGCACCC
546 S F T Y K L T A A R R N L A L F Q H H D G V T G T A K D Y V V Q D Y G T
1745 GGTGATATCTTCTGCAAGACCTTCAGATCTTTATGCTTAAGCAATCTGAAGTTCTTCTTGGGATCCGCGACGAGAAGAAAAATCTGATCAATCCCATCATTTT
582 R M H T S L Q D L Q I F M S K A I E V L L G I R H E K E K S D Q S P S F P
1854 CGAGGACAGGCAATGAGATCAAGATGATGCTCGGCGCTTCAAGCCAAATGCTGCGCGGAAGGAATTCGACACAGTTATCTTCAATCCATCAGAACAG
618 E A E Q M R S K Y D A R P V H K P I A A R E G N S H T V I L F N P S E Q
1963 ACAGAGAGGAGGCTGCTGAGCGGTTGTTGTTAACCAGGCTCAAACTCTCGGTTTGGACTCAAACTGGACTTGTGTCTTACGCAAAATTTCTCTGAAGTGCAGCAGGACG
655 T R E E V T V V V N R A E I S V L D S N W T C V P S Q I S P E V O H D
2072 ATACCAAACTATTCAACGGGAGACATCGGCTTACTGGAAGCTTCCATCCAGCTCTTGGTCTGAGAACATATTTCATTGCTAATGGGAATGTCCAGTGTGAGAAAGC
691 D T K L F T G R H R L Y W K A S I P A L G L R T Y F I A N G N V E C E K A
2181 TACTCGCTCAAACTCAATACGCTTCTGAGTTTGACCCATTTCTTGTCTCTCTCATATTCTGCTCCAACTCGACACGAGCTTACTGAGATCCGAATGAACAT
727 T P S K L K Y A S E F D P F P C P P P Y S C S K L D N D V T E I R N E H
2290 CAGACTCTTGTGTTGATGTGAAGAACGGATCACTCGGGAAGATAGTCCATAGAAACGGATCAGAGACTGTTGGGAGAAGAGATAGGTATGTACTCTAGTCCAGAGA
764 Q T L V F D V K N G S L R K I V H R N G S E T V V G E E I G M Y S S P E
2399 GTGGAGCTTACCTGTTCAAAACAGATGGTGAAGCTCAGCCAATTTGTTCAACTGATGGACATGTAGTCACTCTGAGGGTCTGCTGGTTCAAGAAGCTCTTCTTACCC
800 S G A Y L F K P D G E A Q P I V Q P D G H V V T S E G L L V Q E V F S Y P
2508 TAAAACCAATGGGAGAAATCACCCCTCTCTCAGAAAATCGCTTTTACACTGGAGGTAAATACGCTTCAAGGATGGTGGTGGATAGATATCATGTTGAGCTTCTT
836 K T K W E K S P L S Q K T R L Y T G N T L Q D Q V E I E Y H V E L L
2617 GGTAAATGATTTTGTATGACCGGGAATGATTGTCGGGTACAAGACTGATGTTGACAACAAGAGCTTCTTATTGATCTCAATGGTTTCCAAATGAGCAGGAGCAAAA
873 G N D F D D R E L I V R Y K T D V D N K K V F Y S D L N G F O M S R R E
2726 CTTATGATAAGATCCCTCTTCAAGGAACTACTACCAATGCCATCTCTCGATTATCCAAGGATCCAATGGTCAGAGATTCTCGGTGCACTCTCGTCAATCTCTCG
909 T Y D K I P L Q G N Y P M P S L A F I Q S N G O R F S V H S R O S L G
2835 TGTGCAAGCTCAAGAGGGTTGTTGGAGATTATGCTGGACAGACGTTGGTTGCTGATGACGGACGGGCTAGGGCAAGGTTGATGGATAACCGCGCAATGACC
945 V A S L K E G W L E I M L D R R L V R D D G R G L G Q G V M D N R A M T
2944 GTGGTATTTCACTTCTTGGGAACTAACATTTCTCAAGCAGACCTGCTTCAACACTAACCCGAGGAACCTTCTGCTTCTCTCACCTCATAGGTGCTCACTTAA
982 V V F H L L A E S N I S Q A D P A S N T N P R N P S L L S H L I G A H L
3053 ACTACCCCAATAACACATTTCATGCAAGAAACCGCAAGACATATCTGCGGTGTTCCACAAATACGGTTCTTTCCTTCTTACGCAACCGTACCATGTCGACCTCCA
1018 N Y P I N Y P I A K K P Q D I S V R V P Q Y G S F A P L A K P L P C D L H
3162 CATTTGAAATTTCAAGGTTCTCTGCTCCATCCAAATCTCTCAGCAATTTGGAAGAACCAAGGTTGCTTCTTATCTCAATAGACGAGCTTGGGATTCAGCTTAT
1054 I V N F V P R P S K Y S Q L E E D K P R F A L I L N R A W D S A Y
3271 TGCCATAAAGGAAGACAACTAACTGCACAAGCATGGCTAATGAACAGTAACTTTTCCGACATGTTCAAAGATCTTGCAGCTTCAAAGGTTAAACCACTTCACTGA
1091 C H K G R Q V N C T S M A N E P V N F S D M F K D L A S K F K P T S L
3380 ATCTCTGCAAGAGATATGAGGATTCTTGGGTACGATGACCAAGAGCTACCTCGAGATAGTTACAGCCACGGGAAGGAGCTGTCTCGATCTCTCCATGGAATACG
1127 N L L Q E D E M E I L G Y D D Q E L P R D S S O P R E G R V S I S P M E I R
3489 AGCTTATAGCTTGAACCTCGACCTCACAAGTGA
1163 A Y K L E L R P H K

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C. elegans Mannosidase II (NM_073594)

1 ATGGGAAAACGCAATTTCATATTATTCCTATGTTGGGAGTCTTTCTCACCGTATCACTCTATTGTGACAATGGAATGAACCGGAGCTGAAGCGCTCACCAAAACGCA
1 M G K R N F Y I L L C L G V F L T V S L Y L Y N G I E T G A E A L T K R Q
111 AGCAAAATGATTACCGCGGAAAAATCGAAATNTGGAGCATGTAGCAGAGAAGAAATGGGAAGACGATAGACCGCTTGGAAACGAAGTGTCAACGACGAAAAAGTGTAAAAAT
37 A N D L R R K I G A N L L E H V A E E N G R T I D R L E Q E V Q R A K A E K
221 CGGTGATTTTGTATGAAGAAAAGAAAAACGGAAGAAAAGAGTACAAAAAGAGAAAAAGATGTCCACGATTCAGGTTCGAGGAAATCGTGGTGAATGGGTCTAT
74 S V D F D E E K E K E E E E E E E E E E V A P V P V R G N R G E M A H
331 ATTCATCAAGTAAAGCAACATCATCAAGCCCACTCATGATCAAGAGATGTTTGGAAATAGAGAAAACGTGAGCATTCGTCATTGAGCATGCAGATGCTCGATCTCTA
111 I H O V K Q H I K P T P S M K D V C G I R E N V S I A H S D L Q M L D L Y
441 TGACACCTGGAGTTTGGAAATCCAGACGGAGGTGTATGGAACCAAGGATGGAAATTAATACGATGACAGAAAAGTCAAAATCTCTCCACGTTTGGAGTTTATGTGTA
147 D T W K F E N P D G G V W K Q G W K I E Y D A E K V K S L P R L E V I V
551 TACCTCATCTCATGTGATCCCGATGGATTATGACTTTCGAAGAGTATTACACACAGAAAACGTGCAATATTTCTGATGGAATGGCTAAACATTTCGCAGAAAAGAAC
314 I P H S H C D P G W I M T F E E Y Y N R Q T R N I L D G M A K H L A E K A
661 GAAATCGCGTTTATATGACGAAATATCATTTTGCAAATTTGGTGAGACAGGAGCATGAAATAAAAAGAAAGTTAAAGGATATTGGAAGCAGGAAAAGTTTGA
221 E M R F I Y A E I S F F E T W R W R D Q A D E I K K V K G Y L E A G K F E
771 AATTTGTACTGGCGGATGGGTTATGACAGATGAAGCTAATGCACATTATCACTCAATGACTGAATTTGTCAGGACATGAATGGATTCAAAATCATTGGGAAAAA
257 I V T G W V M T D E A N A H Y H S M I T E L F E G H E W I Q N H L G K
881 CGCGCATCCCAATCTCATTTGGTCAATGATTCATCGGTTTACCCATCAATGCACATTCTTCACTTCTGCTAATATAACCAATGCTGAATTCGCAAGATTCAT
294 S A I P Q S H W S I D P F G L S P S M P H L L T S A N I T N A V I Q R V H
991 TATTGGTGAACGTCGAGTCTCTGTAAGAAAATCTGAAATTTCTAGGACGAAATTTGGATCAACTGGACATCTTGCTTCGATTCACATTTATGCGCTTCTA
331 Y S V K R E L A L K K N L E F Y W R Q L F T G S T G H P D L R S H I M P F Y
101 CTCTTACGATATACCTCATACGCTGTGGCCGAGAACCGTCTGTTTCTGTCAATTCGATTTCGTAAGATGCCAGAGGTGGAAATCATGTGATTTGGGGAATCCCTCCAC
367 S Y D I P H T C G P E S V C C Q F D F R M P E A G G K S C D W G I P P
1211 AGAAAATTAACGATGACATGTGGCTGCACAGAGCTCAATGATTATGATCAATATAGAAAGAAAAGTCAACTTTTCAAGAAATATGATGATTTTCAACCACTTGGAGAT
404 Q K I N D N V A H R A E M I Y D Q Y R K S Q L F K N H V I F Q P L G D
1321 GATTTGAGTACGATGATTGTTGAATGGAATTCACAAATTAAGAAATTTGCGAATACATGAATTCAAATCAGAATGGAATGTTTATGCTCAATTCGG
441 D F R Y D I D F E W N S Q Y E N Y K K L F E Y M N S K S E W N V A H Q F G
1431 AACTCTTTCTGATTATTTCAAGAAGCTTGATACTGCAATTTCTGCGTCTGGCGAGCAATTCGAATTTTCTGGAGATTCTTCACTTATCGGACAGAGATCATTT
477 T L S D Y F K K L D T A I S A S G E Q L P T F S G D F F T Y A D R O O H
1541 ATGGAGTGGATCTTCACTTCGCTGCTATTAACACAGCTGATCGGGTTTCCCAACATTATTAAGATCAGCTGAAATCGCTTTACCTTGCAAATTTGAAGAA
514 Y W S G Y A C T T S R P F Y K Q L D R V L O N Y L R S A E I A F T L A N I E E
1651 GAAGGAATGGTGAAGCGAAAATTTTGAAGAGCTTGACTGCTGCAGAGCTCTTCACTTTTCAACATCAGCATGGTGTAACTGGTACGCGAAAAGATCAGTCGT
551 E G M V E A K I F E K L V T A R R A L S L F Q H M D G V T G T G C K A D H V V
1761 CTGGATTATGGTCAGAAAATGATTGATGCTTTGAACCGATGTGAGGATATTCTTTCGGAAGCTCTGTTGATTGCTGGGAATGATTCAACGAATTAAGATCGACATGG
587 L D Y G Q K M I D A L N A C E D I L S E A L V L L G I D S T N K M Q M
1871 ATGACGATAGAGTTAATGAAACCTTACCCGAAAAACGTCTATAAAATTTGGGAAAAACGTGATTTGTTCAATCTTTATCTAGAAATCCGACAGGACAAATTTGT
624 D E H R V N E N L L P E K R V Y K I G O N V L F N T L S R N R N E P I C
1981 ATTCAGTTGATTCTTGACGCTGGTGTCCGAGCTGATCTCCAATTAAGAAACAAAGTTTCCCGGTTATTGCATATGATGAAGAGAGAAAACGCTTGTGTCAA
661 I Q V D L D A G V E A D P P I K K Q Q V S P V I A Y D E E K K T L V V K
2091 AAAACGGAATATTGCAACTTTGCTTCATGTTATCACTTGACCAATGGAGTCTGTCAGTTTCAGACTGTGAAAATCAACAACATCCAAAGTTGAAATATCACCATA
697 N G I F E L C F M L S L G P M E S V S F R L V K N T T T S K V E I I T N
2201 ATGCGGAGCAATTTCAAGAAAACAAAGTTTAAATCTTCACTCACTCTGGAGACTTTACTGTGAAAACGACAAAAGTTGAAGCTGAATTTGATGGAGAAATGGAATGATT
734 N A A E F K E T S F K S S T S G D F T V A N N D K V E A E F D G E N G M I
2311 AAAAGAGCTACCACTTGTGTTGATGATAAACCAATGATTGAAATCTCACTTATTATTGAGGACCGGAAGTCAAGAGAAAAGTTCCGAATTCGAAATGGAATGAAGACAA
772 K R A T S L V D D K P I D L N S H F I H Y G A R K S K R K F A N G N E D N
2421 CCGCGCTGGCGCATACCTGTTCTCTCCGATGGAGAGCTAGAGAATCAAAAAACATCAAGTATGGATTTGTAAGAGGAGAGATGTTTCAAAAAGTGTTTGCAA
807 P A G A Y L F L P D G E A R L K Q S S D W I L V K G E V Q K V F A
2531 CTCGAAAACATGATCGAAATTTGCAACGCTACACATTTATCAAGGGCTTCCATGGATTGATTGGATAATGAAGTTGATGATCGTTCCAAGGAGAAATTCGAGTTG
844 T P N N D L K I L O T T G T T Y L Q G L P W I D L N E V D V R S K N E F L
2641 GCATCGAGTTGATTCTTCTAGTAATAGTGGTGATGAGTTTCTCACTGATCTCAATGGAATGCAAAATGATAAAAAGGAGACGACAACTAAATACCAACACAGGCCAA
881 A L R F S S S V N S G D E F F T D L N G M Q M I K R R R Q T K L P T Q A N
2751 TTTCTATCCCATGCTGTGGTCTTTACATTTGAAGACGATACTACCAAGATGTCATTCATTTCGGACAGGCTCTCGGAGTTAGCAGTCTCTCTCGGACAAATGAAA
917 F Y P M S A G V Y I E D D T T R M S I H S A Q A L G V S S L S S G Q I E
2861 TAACTGTTGATCGACCATAGTTTACATGACCAACAGAGGCTTTCAGCAAGGAGTTAGACACAACAAACAGTTCACATTTCCGATTGTTATGAGGCGAGTGTCT
954 I M L D R R L S S D D N R G L O G V R D N K R T V A H F R I V I E P M S
2971 TCATCGAGTGGTAATAAGAAAGAAACAGGTTGATTTCATTACATGTGGTGTCTCGCTACGTTGGTCTCTTCAATTCCTCTTGTCAAAATGATTGGAGATGCAAC
991 S S S G N K E E R V G F H S H V G H L A T T W S L H Y P L V K M I G D A T
3081 ACCAAAAATCTATTTCCTGAAAAATGTGGAACAGAGCTGAACGTGACCTGCACTAGTGACATTTAGAACCTGGGATCGCGGACAACTACGAGGACCAACGAAAGAT
1027 P K S I S K N V E Q E L N C D L H V T F R T L A S P T T Y E A N R
3191 CTCAGCGAGCTGAGAAAGAACGAGCGATGTTGATGATGATAGATTTCTTCAGAGCTAGATCCAGGCTTACCCTCCGACAGCATGCTGCTTATGCTATGCTATGAAAT
1064 S T A A E K K A A M V M H R V P D C R S R L T L P D C T S C L A T G L E I
3301 GAGCCATCAATTTGATCTGCAGATGAAGTCTGGGAAAAACGCTCACTAACCAATTTTATGAAGGAAAACAGGCTGAACAAATTCGCACTCCAACCAACGATATTC
1101 E P L K L I S T L K S A K K T S L T N L Y E G N K A E Q F R L Q P N D I S
3411 CAGTATTCTGTATCATTTTAA
1137 S I L V S F

FIG. 27

Ciona intestinalis mannosidase II (AK116684)

[illegible]

FIG. 28

Drosophila mannosidase II (X77652)

1 ATGTTGCGCAATACGTGGGGGTTGCGTTGGTAATTTGCTCCGGCTGCTCTGGTITTTCTCAGCCTGTACATAATCTCTCAATTTTGGCGCGCCGCGCAGCCACCAGA
2 M L R I R R R F A A L V I C S G C L L Y F L S L Y I L N F A A T A T Q
3 110 TAAAGCCCAACTATGAGAACATTTGAGAACACCTGCATGAGCTGAGGAAATGCTTTGCAGGAGCAGGGGAGGATGCGGAATCTCAGGGGCGCTCTGGCAGAAATC
4 37 I K P N Y E N I E N I E N L H E L E N G L Q E H G E E M R N L R A R L A K T S
5 219 CAATCGGCAGCATCCAATAAGACTCTCACTTAAAGTGCTGTCTCCCGAGGCGAGGCAATGCCAAGATGTGGTCCAAGAGCTGCCCAATGTGGATGTACAGATGCTG
6 73 N R D D P I R P L K V A R S P R P G Q C Q D V V Q D V P N V D V Q M L
7 328 GAGCTATACGATCGCATGTCTTCAAGGACATAGATGGAGGCGTGTGGAAATCAGGGCTGGAACATTAAAGTACGATCCACTGAAGTACAAACGCCCATCACAAATCAAAG
8 110 E L Y D R M S F K D I D G G V W K G W N I K Y D P L K Y N A H H K L K
9 437 TCTTGGTGTGGCCGCACTCGCACAACGATCTCGGATGGATTACAGAGCTTTGAGGAATATTACGAGCAGCAGCACAAGCAGCATCTCTGTCCAATGCACTACGGCATCTGCA
10 146 V F V P H S H N D P G W I Q T F E E Y Y Q H D T K H I L S N A L R H L M
11 546 CGACAATCCGAGATGAAGTTCATCTGGGCGGAAATCTCTACTTTGCTCGGTCTATACGATTGGGAGAGAAACAAAAGCTGCAGATGAAGTCCATTGTAAAGAAT
12 182 D N P E M K F I W A E I S Y F A R F Y H D L G E N K K L Q M K S I V K N
13 655 CGACAGTTGGAATTTGTGACTGGAGATGGGTAAATGCGCGGACAGGCCAACTTCCACTGGGCAAAAGCTATGCTGCAGTGCACCGAAGGGGCAAACTGGTTGAAGCAAT
14 219 G O L E F V T G G W V M P C D E E T S S H W R N V L L Q L T E G O T W L K Q
15 764 TCATGAATGTCACACCACTGCTCTGGGCACTCGATCTCTGGACACAGTCCCACTACCGGTACATTTTGCAGAAAGTGGTTTCAAGAAATATGCTTATCCAAAG
16 255 F M N V T P T A T S W A I D P F G H S P T M P Y I L Q K S G F K N M L I O R
17 873 GAGCAGCTATTCTGGTTAAGAGGAACTGGCCCAACGCGACAGCTTGAGTTCTGTGGCGCCAGATCTGGGCAACAAAGGGGACACAGCTCTCTTACCACCATGATG
18 291 T H Y S V K K E L A Q O R L E F L W R Q I W D N K G D T A L F T H M M
19 982 C C C T T A C T C G T A C G A C A T T C C T A C T C T G G T C C A G A T C C A A G G T T G C T G T C A G T T C G A T T C A A A C G A A T G G G C T C C T T C G G T T G A G T T G C C A T G G A A G G
20 328 P F Y S Y D I P H T C G P D P K V C Q F O F K R M G S F Q L S C P W K
21 1091 TGCGCGCGGTACAACTCAGTGAATCAAAATGTGGCAGCAGCTCAGATCTGCTGGTTGATCAGTGGAGAAGAAGGGCGAGCTGTATCGCACAACCTGCTGCTGATTC
22 364 V P P R T I S D N V A R S D L L V D Q W K K A E L Y R T N V L L I P
23 1200 GTTGGGTGAGCACTTCCGCTTCAAGCAGAACACGAGTGGGATGTGCAGCGCGTGAATCGAAAGGCTGTGCAACACTCAACAGCGAGGCCCATCTCAATGTCCAG
24 400 L G D D F R F K T N T E W D V Q R V N Y E R L F E H I N S Q A H F N V Q
25 1309 GCGCAGTTGGCAGCACTCAGGAATACTTTGATCGAGTGCACGAGCGGAAGGGCGGCAAGGCGAGTTTCCACGTAAAGCGGTGACTTTTACATACCGCGGATC
26 437 A O F G T L Q E Y F D A V H Q A E R A G Q A E F P T L S O D F F T Y A D
27 1418 GATCGGATAACTTTGGAGTGGCTACTACACTCCCGCCCGTATCATAAAGCGCATGGACCGCGCTCTGATGCATATGTACGTGCAGCAGAAATGCTTTCCGCTGGCA
28 473 R S D N Y W S G Y Y T S R P Y H K R M D R V L M H Y V R A E M L S A W H
29 1527 CTCTCGGAGCGGATGGCCCGCATCGAGGAACCTCTGGAGCAGGCGCCGAGGAGCTTCATTGTTCCAGCAGCAGCGGATATAACTGGGACAGCAAAAGCGCATGTA
30 509 S W D G M A R I E R L E Q A R R E L S L F Q H H D G I T Q T A K H V
31 1636 GTCTGCGACTACGAGCAAGCGATCGAGGAAGCTTTAAAGCCTGTCAAAATGGTAATGCAACAGCTCGGTCTACGGATTGCTGACAAGAGCCTCCATCTACAGTCCGGACT
32 546 V V D Y E Q R M Q E A L K A C Q M V M Q Q S V Y R L L T K P S I Y S P D
33 1745 TCAGTTTCTCGTACTTTACGCTCGACGACTCCCGCTGGCCAGGATCTGTTGTGGAGGACAGTGCAGAACCCATAAATCTGGCGAGGATATACCTGCCCTCCAAGCATG
34 582 F S F S Y F T L D S R W P G S G V E D S R T I L G E D I L P S K H V
35 1854 GGTGATGCAACAACCTTCCCGCATCGCGGAGCAGCTGGTGGACTTTATGTATCAGTCCGTTTGAAGCGTTACCGACTTGGCAACAACTCCGGTGGAGGCTCAG
36 618 V M H N T L P H W R E Q L V D F Y V S S P F V S T V A N N P V E A Q
37 1963 GTGTCCCGGTTGGAGCTGGCAGCAGACACTCAAAAGACTATCCACCACAAGGCTCCACCACCAAGTACCGCATCATCTTCAAGGCTCGGTCGCCGCCCATG
38 655 V S P V W S W H H D T L T K T I H P Q G S T K Y R I I F K A R V P P M
39 2072 GCTTGGCCCACTACGTTTAAACCATCTCCGATCCCAAGCCAGAGCAGCTCGTATGACATCGAATCTTGTCTCGTAAAAACCCGAGCTCGTTACCATTTGGCCCAATA
40 691 G L A T Y V L T I S D S K P E H T S Y A S N L L R K N P T S L P L Q O Y
41 2181 TCCGGAGGATGTGAAGTTTGGCGACTCTCGAGAGATCTCATTCGGCGTTGTGAACGACCACTTGGCCCTTTCCGAGCAGGGGTCTCTTAAGTCCATTACGTTACT
42 727 P E D V K F G D P R E I S L R V G N O P T L A F S E Q G L L K S I Q L T
43 2290 CAGGATAGCCACATGTACCGGTGCACTCAAGTCTCTCAAGTATGGCGTTGCATCGCATGGCGATAGATCCGTTGCCATCTCTGTTCTGCCCAATGGACGAGCTTCG
44 764 Q D S P H V P H F K L K Y G V R S H G D R S G A Y L F L P N A T G
45 2399 CAGTCAGACTTGGCCAGCCAGTGGTCTGGTGAATGAAGGGCAAACTGGAGTCGTCGTCAGCGTGGGACTCCGAGCGTGGTGACACCAAGCATATCGCGGTTGGTGC
46 800 P V E L G Q P V L V T K G K L E S S V S V G L P S V H H Q T I M R G G A
47 2508 ACTGAGATTGCAATCTCGTGGATATAGGCTCACTGGCAACAACGAGAGCTGTGATGGCTTGGAGACGCATATCGACAGCGGGCGATCTCTACACGGATCTCAAT
48 836 P E I R N L V D I G S L D N T E I V M R L E T H I D S G D I F Y T D L N
49 2617 GGATTGCAATTTATCAAGAGCGCGCGTTGGACAAATTAACCTTTGCAGGCGCAACTATTATCCCATACCTTCTGGTATGTTTCAATGAGGATGCCAATACCGGACTCACTC
50 873 G L O F I K R R R L D K L P L Q A N Y Y I P S G M F I E A N T R L T
51 2726 TCTCAGCGGTCCAACCTGCTGGTGGATCTCTCTGGCTCTGGGCGAGCTAGAGATTATGCAAGATCGTCCGCTGGCCAGCGCATGATGAACCGCGGCTGGGACAGGGTGT
52 905 L T G Q P L G G S L A S G E L I M O D R R L A S D E R G L G O O V
53 2835 TTTGCAACAAAGCCGCTGCTCATATTTATCGGCTGGTCTGGAGAAAGGTTAAACAACTGTGTCGAGCGCTCAAGCTTATCTCTGCGCGGCTATTGACAAGTCCCCA
54 945 L D N K P V L H I Y R L V L E K V N H C V R P S K L H P A G Y L T S A A
55 2944 CACAAAGCATCGCAGTCACTGCTGGATCCACTGGACAAGTTTATATTCTGCTGAAATGAGTGGATCGGGGACAGGGGCAATTTGGTGGCGATCACTCTTCCGCTCGTG
56 982 H K A S O S L L D L D K F I F A E N E W I G A Q G Q F G D H P S A R
57 3053 AGGATCTCGATGTCTCGGTGATGAGACGCTTAAACAAGAGCTCGGCAAAAACCCAGCGAGTAGGCTACGTTCTGCACCGCAACCAATCTGATGCAATGGCGGACCTCAGA
58 1018 E D L D V S V M R R L T A K S S A C T Q R V G Y V L H R T A N L M Q C G T P E
59 3162 CGAGCATACACAGAAGCTGGATGTGTCACCTACTGCCGAATGTGGCGAGATGCAGCGCAGCAGCTGACTTCTGTCAGAAATTTGGAGCATTTGGAGCATGGCATGGTG
60 1054 E H T Q K L D V C H L L P N V A R C E R T T L T F L Q N L E H L D G M V
61 3271 CGCGCGGAAGTGTGCCCATGGAACCGCGCTTATGTGAGCAGTCACTCAAGCTGA
62 1091 A P E V C P M E T A A Y V S S H S

FIG. 29

Human mannosidase II (U31520)

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1 ATGAAGTTAAGCCGCGAGTTACCGTGTTCGGCAGTCCGATCTTCTGTGGTGATTCTTCGCTCTACCTGATGCTGGACCGGGGTCACTTAGACTACCCAGGAACC
2 M K L S R Q F T V F G S A I F C V V I F S L Y L M L D R G H L D Y P R N
110 CCGCCGCGGAGGCTCTTCCCTCAGGGCCAGCTCTCAATGTTGCAAGAAAAATAGACCAATTTGGAGCGTTTGCTAGCTGAGAATAATGAGATCATCTCAAATATTAG
117 P R R E G S F P Q G Q L S M L Q E K I D H L E R L L A E N N E I I S N I R
219 AGACTCAGTCATCAATTTGAGTGAGTCTGTGGAGGATGGTCCGAAAAGTTCACAAAGCAATTTAGCCAAAGGTGCTGGCTCAGATCTTCTGCCCTCACAATATCCCTC
226 D S V I N L S E S V E D G P K S S O S N F S Q G A G S H L L P S Q L S L
328 TCAGTTGACACTGCAGACTGTCTGTTGCTTCACAAAGTGGAGTCACAATTCAGATGTCAGATGTTGGATGTTTACAGTCTAATTTCTTTTGACAATCCAGATGGTG
335 S V D T A D C L F A S Q S G S H N S D V Q M L D V Y S L I S F D N P D G
437 GAGTTTGGAGCAAGGATTGACATTACTTATGAATCTAATGAATGGGACACTGAACCCCTTCAAGTCTTGTGGTGGCTCATTCCCAATACGACCCAGGTGGTGAA
444 G V W K Q G F D I T Y E S N E W D T E P L Q V F V V P H S H N D P G W L K
546 GACTTTCAATGACTACTTTAGAGACAAGACTCAGTATATTTTAAATACATGGTCTTAAAGCTGAAAGAAGACTCACGGAGGAAGTTTATTTGGTCTGAGATCTTTAC
553 T F N D Y F R D K T Q Y I F N N M V L K L K E D S R R K F I W S E I S Y
655 CTTTCAAAGTGGTGGGATATTAGATATTGAGAAGAAGTCTGTTAAAGTTTAAATAGAAAATGGTCAAGTGTGACAGGTGGCTGGGTTATGCTGATG
662 L S K W W D I I D I Q K K D A V K S L I E N G Q L E I V T G G W V M P D
764 AAGCTACTCCACATTTATTTGCCCTTAATTTGATCACTAATTTGAAGGACATCAGTGGCTGGAAAATAATATAGGAGTGAACCTCGGTCCGGCTGGGCTATTGATCCCTT
771 E A T P H Y F A L I D O L I E G H Q W L E N N I G V K P R S G W A I D P F
873 TGGACACTCACCAACATGGCTTATCTTAAACCGTGGTGGACTTTCTCATGCTTATCCAGAGAGTTCATTATGCAGTTAAAAAACTTTTGCATGCCATAAAAACA
880 G H S P T M A Y L L N R K A G L S H M L I O R V H Y A V K K H F A L H K T
982 TTGGAGTTTTTTGGAGACAGAATTGGGATCTGGGATCTGTACAGATATTTTATGCCACATGATGCCCTTCTACAGCTATGACATCCCTCACACTGTGGACCTGATC
989 L E F F W R Q N W D L G S V T D I L C H M M P F Y S Y D I P H T C G P D
1091 CTAAAAATGCTGCCAGTTTGAATTTAAACGTTCTCTGGAGGAGAGTTTGGTTGTCCCTGGGGAGTCCCCCAGAAAACAATACATCTCGAAATGTCCAAAGCAGGCG
1098 P K I C C Q F D F K R L P G G R F G C P W G V P P E T I H P G N V Q S R A
1200 TCGGATGCTAGTACAGTACCGAAAGTCAAGCTTTTCCAGCAAAAGTCTTCTGGCTCCACTAGGAGATGATTTCGGTACTGTGAATACACCGGAATGGAT
1207 R M L L D Q Y R K K S K L F R T K V L L A P L G D D F R Y C E Y T E W D
1309 TTACAGTTTAAAGATTATCAGCAGCTTTTGAATATGAATTTCTCAGTCCAAGTTTAAAGTTAAAGATACAGTTTGAAGCTTTATCAGATTTTTTGTATCGCTCGGATA
1316 L Q F K N Y Q O L F D Y M N S O S K F K V K I O F G T L S D F F D A L D
1418 AAGCAGATGAACTCAGAGACAGAAGGGCAATCGATGTTCCCTGTTTAAAGTGGAGATTTTTTCACTATGCCGATCGAGATGATCATTACTGGAGTGGCTATTATAC
1425 K A D E T Q R D K G O S M F P V L S G D F F T Y A D R D D H Y W S G Y F T
1527 ATCCAGACCTTTTACAAACGAATGGACAGAATCATGGAATCTCTTAAAGGCTGCTGAAATTTCTTACTATTTCCGCTCAGACAAAGCTCACAAATACAGATAAAT
1534 S R P F Y K R M D R I M E S H L R A A E I L Y F A L R Q A H K Y K I N
1636 AAATTTCTCTCATCATCTTACACGGCACTGACAGAAGCCAGAGGAATTTGGGAGTGTTCACACATCATGATGCTATCACAGGAAGTCCAAAGAGTGGTGGTTG
1643 K F L S S S L Y T A L T E A R R N L G L F Q H H D A I T G T A K D W V V
1745 TGGATTATGGTACCAGACTTTTCTTCTGTTAATGGTTTGGAGAAATTTGGGAAATTTCTGCAATTTCTTCTTATTGGGAGGCAAACTCACATACGACTTACTCT
1752 V D Y G T R L F H S L M V L E K I I G N S A F L L I G K D K L T Y D S Y S
1854 TCTGATACCTTCTCGGAGATGGATTGAAACAAAAATCACAAGATCTCTGCCACAAAAAATAATAAGGCTGAGTGCCGAGCAAGCTTCTGGTCTATAAT
1861 P D T F L E M D L K Q K S Q D S L P O K N I I R L S A E P R Y L V V Y N
1963 CCTTTAGAACAGACCAATCTCGTTGGTCTCAGTCTATGTGAGTTCCTCCGACAGTCAAGGTGTTCTCTGCTTCAGGAAACCTGTGGAAGTCAAGTCAGCGAGCTTT
1970 P L E Q D R I S L V S V F V S S P T V Q V P S A S G K P V Q V S A V
2072 GGGATACAGCAATACTATTTAGAAACAGCTATGAGATCTCTTTCCAGGACATATACCGCCATTGGGACTGAAAGTGTATAAGATTTTGAATCAGCAAGTTCAAA
2079 W D T A N T I S E T A Y E I S F R A H I P P L G L K V Y K I L E S A S S N
2181 TTCACATTTAGCTGATTATGTTGTATAGAATAAAGTAGAAGATAGCGGAATTTTACCATAAAGAAATATGATAAATCTCAAGAACGTATAACACTAGACAACTCC
2188 S H L A D Y V L Y K N K V E D S G I F T I K N M I N T E E G I T L E N S
2290 TTTGTTTACTTGGTTGATCAAACTGCACTTATGAAGCAATGATGACTAAAGAAAGTGGTAAACACCATGAAGTAAATGTGCAATTTTATGGTATGGAACCAAA
2297 F V L L R F D O T G L M K Q M M T K E D G K H E V N V Q F S W Y G T T
2399 TTTAAAGACAAAAGTGGTGGCTTCTTCTTACCTGATGGTAAATGCCAAGCCTTATGTTTACACAAACACCGCCCTTGTGAGAGTGACACATGGAAGGATTTATTC
2406 I K R D K S G A Y L F L P D G N A K P Y V Y T T P P F V R V T H G R I Y S
2508 GGAAGTGACTTGTCTTTTGGACATGTTACTCATAGAGTCCGACTATACACATACAGGGAATAGAAGGACAGTCTGTGGAAGTTTCCAATATTGTGGACATCCGAAA
2515 E V T C F F D H V T H R V R L Y H I Q G I E G Q S V E V S N I V D I R K
2617 GTATATAACCGTGAGATTGCAATGAAAATTTCTTCTGATATAAAAGCCAAAATAGATTTTATCTGACCTAAATGGGTACCAGATTCAACTACAATGACATGACCA
2624 V Y N R E I A M K I S S D I K S Q N R F Y T D L N G Y O I Q P R M T L S
2726 AATTGCCCTTCAAGCAATGCTATCCCATGACCAATGGCTATATCCAGGATGCCAAACATCGTTTGACACTGCTCTCTGCTCAGTCATTAGGGGTTTCGAGTTT
2733 K L P L O A N V Y P M T M A Y I O D A K H R L T L L S A O S L O V S B L
2835 GAATAGTGGTCAGATTGAAGTTATCATGGATCGAAGACTCATGCAAGATGATAATCGTGGCCTTGAGCAAGGTATCCAGGATAACAAAGATTACAGCTAATCTATTTCGA
2842 N S G Q I E V I M D R R L M Q D D N R G L E O G I O D N K I T A N L F R
2944 ATACTACTAGAAAAAGAGTGTGTTAATACGGAACAGAAAAGAGTGGTCAAGTATCTTCTCTCTAGCCACATACTTCTTCTCTCATGAATCATCCAGTCA
2951 I L L E K R S A V N T E E E K K S V S Y P S L L S H I T S S L M N H P V
3053 TTCCAAATGGCAATTAAGTTCTCTCACTACCTTGGAGTGCAGGTTGAATTTCTCTCATTACAGTCTATCTTCCCTTGTGACATTCTGGTTAATTTGAGAACAA
3060 I P M A N K F S S P T L E L O G E F T S P L Q S S L P C D I H L V N L R T I
3162 ACAGTCAAGGTTGGGCAATGGGCACTCCAATGAGGCAAGCTTGAATCTTCCACAGAAAAGGTTGATTGTGGGTTCTCTAGCAAGGACAGGCGCTTTGTTCTTACT
3169 O S K V G N H S N E A A L L I L H R K G G F T D C R F S K G C R F L F C S T
3271 ACTCAGGGAAGATATTGGTACAGAACTTTTAAACAACTTTATTGTCGAAGTCTCACACCTTCTCATCTATCTTGTGATGATTCACCTCCCGGCACTCAGAAATATA
3278 T O G K I L V Q K L L N K F I V E S L T P S S L S L M H S P P G T Q N I
3380 GTGAGATCAACTTGAAGTCCAATGGAATCAGCAATTCGAATCCAGTTCAGGTGA
1127 S E I N L S P M E I S T F R I O L R

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FIG. 30

FIG. 31

Rat mannosidase II (XM_218816)

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1  ATGGCTGTATAGGTGGAGCCAGGGGCAACGGCAGGCGGTGGAAAAAGGAACCTTCCACCAAGGCTATCCGTGGAAGCCAATGACCAATGGCAGCTGCTCAGAACTG
2  MACIGGAQGGQRAVEKEPSHQGYPWKPM TNGSCSEL
109 GCATTGCTCAGAAAAACCGAATGTACTGTACCAGGGATGTGTAGGCCACCCAGGACTGACGTGAAAAACTTCAAGACCAAACTGATCTCAGAGTGTGCTGCTG
37  A L L S K T R M Y C H Q G C V R P P R T D V K N F K T T T D T Q S V P G
217 GTCAGTATGAAGCTGAAAAAGCAGGTGACAGTGTGCGGGCTGCTATCTTCTGTGTGGCCGTCTTTTCCCTGTACCTAATGCTGGACCGAATGACAGTGTATCTCTCC
73  V S M K L K K Q V T V C G A A I F C V A V F S L Y L M L D R V Q H D P A
325 AGACACCAGAATGGTGGGAACCTTCCCGAGGAGCCAAATTTCTGTGCTACGAACCGGATCGAACAGCTGCGGAAGAAAACCATGAGATCATAGCCAT
109  R H Q N G G N F P R S Q I S V L Q N R I E Q L E Q L L E E N H E I I S H
433 ATCAAGGACTCTGTGCTGGAACCTGACAGCCAAATGCGGAGGGCCACCGCCCTGTGCTCCCTACACACAGCCAAACGGCTCTGGGCTGTGCTCCCCGAGCCCGGGCC
143  I K D S V L E L T A N A E G P P A L L P Y H T A N G S W A V L P E P R P
541 AGCTTCTTCTGTATCCCTGAGGACTGCCAGTTTGTCTTGGGGGGCCGGGCTCAGAAGCCAGAGCTACAGATGTTAACTGTCTCAGGATTTGCGCTTGACAAAT
181  S F F S V S P E D C Q F A L G G R G Q K P E L Q M L T V S E D L P F D N
649 GTGGAGGGGGCGGTGTGGAGGCAAGGCTTCGACATCTCTACAGCCCAATGACTGGGATGCTGAAGACCTGCAGGTGTTTGTGGTGCCTCACTCCCAATGATCCA
217  V E G G V W R Q G F D I S Y S P N D W D A E D L Q V F V V P H S H N D P
757 GGTGAAGAGCCAGCAGGCCCCAGCCGAGCGTGCAGGGTGGGCTTTCTGGTGACAGGCGCTGATCAAGACTTTTGACAACTACTACAGGAAACAAACCAACATC
253  G E E P A G P S R S V Q G G L S G D R R W I K T F D K Y Y T E Q T Q H I
865 CTCACAGCATGGTGTCCAAGCTGCAGGAAGATCCCCAGGGCGTTTCTCTGGGCGAAGCTCTCTTCTTCCCAAGTGGTGGGACAACTCAGTCCCCAGAAAAGG
289  L N S M V S K L O E D P R R R F L W A E V S F F A K W W D N I S A Q K R
973 GCAGCAGTTGCAAGGCTGGTGGGAAATGGGCGAGCTGCAAAATGCAACGGGTGGATGGGTGATGCGCAGATGAGGCGCAACTCCATTACTTTGGCTGGTGGGCGAGCTC
325  A A V R R L V G N G O L E I A T G G W V M P D E A N S H Y F A L V G Q L
1081 ATCGAGGGCCCCCGGTACCGAGGGCAGTGGAGCCCTTTGGACACAGCTCCACCATGCTTACCTGCTGCGCCGTGCAACCTGACCAGCATGCTAATTCAGAGG
361  I E G P P P V R R A V D P F G H S S T M P Y L L R R A N L T S M L I Q R
1289 GTGCATTACGCCATCAAGAGCACTTTGCGGGCACTCAGAGCTGGAGTTCAATGCGAGGCGAGCATGGGATTGAGACTCCAGCAGAGCATCTTCTGCCACATGATG
397  V H Y A I K K H F A A T H S L E F M W R Q T W D S D S T D I F C H M M
1297 CCCTTCTACAGCTACGACGCTCCACACAGCTGTGGCCCTGATCCCAAGATCTGTGCGCAGTTGATTTCAAACGCTGCGCGGGTGGGAGAATCAATGTCTTGGAGG
433  P F Y S F S V S P E D C Q F A L G G R G Q K P E L Q M L T V S E D L P F D N
1405 GTGCCCGCCGGGCTATCAGAGGGCAACGTGGCAGACAGGGCAGCCCTGCTCTGGAGCAGTACCGGAAGAACTCCCGGCTGTTTCGAAGCAGTGTCTCTCTGTG
469  V P P R A I T E A N V A D R A A L L L D Q Y R K K S R L F R S S V L L V
1513 CCGCTGGGTGATGACTCCGATATGACAAGCCAGGAAATGGGATGCGCACTTCACTCAACGGCTCTTGACTTCTCAACAGGCGCTTTGACTTCTCAACAGGCGGAGTTCACGTA
505  P L D G D F R Y D K P Q E W D A Q F F N Y Q R L F D F L N S K P E F H V
1621 CAGGCACAGTTTGGGACCTCTCTGAGTATTTGATGCCCTGTATAAGAGGACAGGAGTGGAGCTGGTGGCCGGCTCCAGGGTTTCTGTGCTGAGTGGGCACTTC
543  Q A Q F G T L S E Y F D A L Y K R T G V E P G A R P P G F P V L S G D F
1729 TTCTCTATGCTGACCCGGGAGGACCACTACTGGACAGGCTATTACACTTCCCGGCTTCTATAAGAGCTGGACCGCGTGTAGAACTCACTCTTGTGGGGCAGAG
577  F S Y A D R E D H Y W T G Y Y T S R P F Y K S L D R V L R G A E
1837 GTTCTATACAGCTGGCTTTGGCGCATGCCCGCCCTTCTGCACTGACTGCCAGTATCCGCTGTCTGATTACGCTGTCTGACCGAAGCTCGCTGTACACTGGGCTTC
613  V L Y S L A L A H A R R S G L T G O Y P L S D Y A V L T E A R T L G L
1945 TTCACGACCCAGCATGCCATCCAGGAACTGCCAAGGAGGCACTTGTAGTACATATGGGCTCAGGTGCTGCGTTCCTGGTTCAGCTTAAGCAGGTTCATCATCAAT
649  F Q H H D A I T G T A K E A V V V D Y G V R L L R S L V S L K Q V I I N
2053 GCTGCCCACTACTGGTGGTGGGCAAGGAGCACTACAGCTTTGACCTTAGGGCACTTCTCTCAAAATGGTGAGGCGAGGCTGGCGAGCTCTCAGAGCACTTC
685  A A H Y L V L L G D K E T Y S F D P R A P F L Q M V S Q A W R G S Q S T L
2161 CACCCAGCCCGGGCTTGTCTCTGCTGCTGCTTCTGCGCTGCTGCGGCGAGGCTCTAGGTTTGTGGTGGTCTTTAACCCTGGAACAGGCGGCTCAGT
721  H P S A A L V P A A A S A L L P Q R A P R F V V F N P L E Q E R L S
2269 GTGGTGTCTCTGGTCAACTCACCAGGAGTGGAGTCTTTCAGAGAGGGTCAAGGCTTCTGTGCGATCAGTGTGCACTGGAGTCCGGCACCACCAATGGT
757  V V S L L V N S P R V R L S E E G O P L S V Q I S V O I S W S A T N M V
2377 CCGATGTCTACAGGTGTCAAGTGTCTGCGCTGCTGCGCCCTGCCAGCCCTGGGCTGGGTGTGCTGCACTGCGAGCCAGATCTCGATGGACCTACACACTGCACTCTCGGTG
793  P D V Y Q V S V P V R L P A L G L G V L Q L O P D L D G P Y T L Q S S V
2485 CATGTCTACCTGCAAGGCTGAACTGTCTGTGACAGGCAACCAACTTCCCTCTCGGTGTGGAGTCCGGGACCAAGTGTGCGCATCAGCAATCGATACATG
829  H V Y L N G V K L S V S R Q T T F P L R V V D S G T S D F A I S N R Y M
2593 CAGGTCTGTCTCCGGCTTACTGGGCTTCTCAAGAGGCTCCGAGCTGTGGAGCAAGAGGAGGAAACAGCAGGTGGACATGAAGCTCTTGTCTATGCAACCCGACCA
865  Q V W F S G L T G L L K S V R R V D E E Q E Q Q V D M K L F V Y G T R T
2701 TCAAGGATAAGAGTGGTGGCTACCTCTTCTGCTGATAACAGGCTAAGCCCTATGTCTCTCAAGAACTCTCTGTGCTGCGGTACCGAAGGCTCTTCTTCTCA
901  S K D K S G A Y L F L P D N E A K P Y V P K K P P V L R V T E G P F F S
2809 GAGGTGGCTGGCTATTATGAGCACTTCAACCAAGTATTGCACTTACAACTGCCAGGGGTAGAGGGGCTGTCTCTGGAGTGTGCTTTCAGGTGGACATCAGGAC
937  E V A A Y Y E H F H Q V I R L Y N L P G V E G L S L D V S F Q V D I R D
2917 TACGTGAACAAGGAGTACGCTTCCGCTCCACACAGACATCGACAGCCAGGGCACTTTCTTACAGACCTCAATGGCTTTCAGGTACAGCCCGGAAATGATCTGAAG
973  Y V N K E L A L R I M T D I D S O G T T F T D L N G F Q V O P R K Y L K
3025 AAGTGTGCTTCCAGGACACTTCTACCTATGCACTGATGCGCTTACCTAGCAGGATTCACAGGCGGCTCACGCTGCACACTGCTCAGGCTCTGGGTGTCTCCAGC
1009  K L P L O A N F Y P M P V M A Y I O D S O R R L L T H T A Q A L G V S S
3133 CTCGGCAATGGCAGCTGGAGGTATCTTGGACCGAAGGCTAATGCGAGGATGACAAACCGGGACTAGGCCAAGGGCTCAAGACAAAGATCACTGCAAGCATTTT
1045  L G N G O L E V I L D R R L M O D D N R G L G O G L K D N K I T C N H F
3241 CGCCTCTGTGTAGAACCTGAAACCTGTATGAGCCCTGAGGCTCAACAGGAGCGCTTACAAGCTACCCGCTCCTCAGCCACATGCTTCACTCACTCAACACA
1081  R L L L E R T L R S E P V O G E R S T S Y P S L S H M T S M Y L N T
3349 CTTGCTGTGCTTACCGGTGGCCAGAGGAGGACAGCCAGCCCACTTGCAGCTTCTTCCACCTCTGGCTTCTCGGTGCCCTGGCATTTCCATCTGCTCAATCTG
1117  P P L V L P V A K R E S T P L H S F H P L A S P L F L H L L N T
3457 CGCATGCTCCCCCGGAGGTGAGTGTCCCGCTCCGCTGCAATCTCACCATCAGGCTGAGCTTGTCTTGGCAGACATGCTGTACCTCCACCGCTTGTGTC
1153  R M L P A E V S V P V R A N P H H Q A E P C L L G R H A A D P P L L S
3565 CTGACTGTCTTCCAGGACACTTCTCCCGCGCTGATGCTGCTCTATCTTACACCGCAAGGGTTTGAAGTGTGGGCTTGAAGCCAAAGACCTGGGCTTCAACTGTACC
1189  L T V F Q D T L P A A D A A L I L H R K G F D C G L E A K N L G F N C T
3673 ACAAGCCAAAGGCAAGTGGGCTTGGGAGGCTCTTCAATGGCTGATGCTATCTCTGAGCCCACTTGTGACTTGTCTATACCTCTGCGCTGCCCTGCCCAAC
1225  T S O G K L A L G S L F H G L D V L F L O P T S L T L L Y P L A S P S N
3781 AGCACTGACATCTCTCTGAGGCGCATGACATCAGCACCTTCCGCTGCGCTTGGTTAG
1261  S T D I S L E P M E I S T F R L R L G

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1 ATGAAGCTGAAAAAGCAGGTGACAGTGTGTGGGGTGCCTCTTCTGTGTGGCAGTCTTCTCGCTACCTCATGCTGCAGCCAGTGCACACAGATCCACCAGCAGAC
110 1 M K L K K V C T V C G A I F C V A V F S L Y L M L D R V Q H D P T R H
110 AGAATGGTGGGAATCTCCCGGGAGCAAAATTTCTGTCTGCAGAACCGCATGTAGCAGCTGGAGCAGTTTGGAGGAGAACATGAGATTATCAGCCATTACAGGA
377 Q N G G N F P R S Q I S V L Q N R I E Q L E Q L L E E N H E I I S H I K D
219 CTCCGTGCTGGAGCTGACAGCAACGACAGAGGGCCGCCGCCCTACTACAGGTCAATGGCTCTGGTGGTGCACCCGAGGCCGCCGCCAGCTCTCTC
73 S V L E L T A N A E G P P A M L P T Y A T V N G S W V V P P E P R P S F F
328 TCCATCTCCCCGAGGAGCTGCGAATTTGCTTTGGGGGGCGGGGGTCAAGAACGAGAGCTGCAGATGCTCACTGTGTCGGAGGAGCTGCCGTTTGACAACGTGGATGGT
110 S I S P O D C Q F A L G G R G O K P E L O M L T V S E E L P F D N V D G
437 GTGTGTGGAGGCAAGGCTTCGACATCTCTACGACCCGACAGCTGGGATGCTGAAGAGCTGCAGGTGTTTGTGGTGGCCCACTCTCACAATGACCCAGGCTGGATCAA
146 G V W R Q G F D I S Y D P H D W A E D L Q V F V P H S H N D P G W I K
546 GACCTTTGACAAGTACTACACAGAGCAGACCCAAACATCTCTAATAGCATGGTGTCTAAGCTGCAGGAGGAGCCCCGGCGGGCTTCTCTGGCAGAGGTCTCTCTC
182 T F D K Y Y T E Q T Q H I L N S M V S K L Q E D P R R R F L W A E V S F
655 TTCGCAAGTGTGGGCAACATCAATGTCAAAGAGAGCGGCACTCGAAGGCTGGTGGGAAACGGGAGCTGCAGATTCGCAAGGAGGCTGGGTGATGCCAGATG
219 F A K W W D N I N V Q K R A A V R R L V N G L O E A I C T A T G G W V M P F
764 AGGCCAATTCCCACTACTTGGCATTTGACCAAGCTCATCGAAGGACACCGTAGGCTGGAGAGAATCTTGGTGAACCCCCGCTCTGGCTGGGCAAGTGACCCCTT
255 E A N S H Y F A L I D O L I E G H Q W L E R N L G A T P R S G A T T W A V D P F
873 TGGATACAGCTCCCACTGCTTACTCTCTGGCCCGTCCCAACTCACCAGCATGCTGATTGAGAGAGTGCACTATGCCATCAAGAAGCGTTTGTCTGCCACCCACAG
291 G Y S S T M P Y L L R R A N L T S M L I Q R V H Y A I K K H F A A T H S
982 CTAGAGTTTCATGTGGAGGAGAGATGGGACTCGGACTCAGGACAGACATCTTCTGTCACATGAGCCCTTCTACAGCTATGACGTCCCCCATACCTGTGGCCAGATC
328 L E F M W R Q T W D S D S T D I F C H M M P F Y S Y D V P H T C G P D
1091 CCAAGATCTGCTGCCAATTTGATTCAAAGCCTGCTTGGTGGGCGCATCAACTGCCCTTGGAGGTGCGACCCCGGGCCATCAGAGAGCCCAAGCTGGCAGAGAGGCG
364 P K I C C Q F D F K R L P G G R I N C P W K V P P R A I T E A N V A E R A
1200 AGCCCTGCTCTGGAGCAATACCGGAAGAAGTCCCAAGCTGTTCCGAAGCAAGCTCTCTGGTGGCTTTGGAGATGACTTCGATATGACAAGCCCGAGGAGTGGGAT
400 A L L L D Q C Y R K K S Q L F R S N V L V L P L G D D F R Y D K P Q E W D
1309 GCCCAGTTCTCAACTACCAAGCGGCTTTGACTTCTTCAACAGAGCGGCTTAACCTCCATGTGCAGGCCAGTTGGGCACTTCTGCACTTTTGTGACTTTGTGCTGACA
437 A Q F F N Y Q R L F D F F N S R P N L H V Q A Q F G T L S D Y F D A L Y
1418 AGAGGAGAGCGGGTGGAGCCAGGGCGCCGGCTCCAGGTTTCTGTGCTGAGCGGGATTTCTTCTCTATGCGAGCCGGAGGACTTACTGGACAGGACTTACAC
473 K R T G V E P G A R P P G F P V L S Y T T S Y A D R E D H Y W T G Y Y T
1527 TTCGCCGCTTCTACAAGAGCTTAGACCGAGTCTCGAAGGCCCACTCGCGGGGGGAGAGGTTCTGTACAGCTTGGGCTGCAGCTCAGGCTCGCCGCTTGGGTCTGGT
509 S R P P F Y K S L D R V L E A H L R G A E V L Y S L A A H A R R S G L A
1636 GGGCGGTACCCACTGTCTGATTTCACCTCTGACCGGAAGCTCGCGCGACATTTGGGGCTCTTCAGCATCAGATGCCATCAITGGCAGCGGCCAAGAGGAGCTGTGGTGG
546 G R Y P L S D F L L T E A R R T L G L F Q H D A I C T I T G T A K E A V Y
1745 TGGACTATGGGCTCAGGCTTCTGCGCTCCCTTGTCAACCTGAAGCAGGTCACTATTTCATGCAGCCCACTATCTGGTGTGGGGACAGGAGACCTACCCTTTGACC
582 V D Y G V R L R S L V N L K O V I I H A A H Y L V L G D K E T Y H F D P
1854 TAGGGCGCCCTTCTCCAAGTGGATGACACTCGTTAAGTACGACGCGCCTCCAGAGCGCAGCGGTGATCGAGCTGGATTCTCGCCACAGTTTGTGGTCTATTCAAC
618 E A P F L Q V D D T R L S H D A L P E R T V I Q L D S S P R F V C G L A
1963 CCACTGGAACAGAGCGATTGACATGGTGTCTGCTCAACTCTCCCGCGTGGCTGTCTTTCGGAGAGGGGTGAGCCCTGGCCGTGCAGATGAGGCGACACT
655 P L E Q E R F S M V S L N S P R V R V L S E E G Q P L A V Q I S A H
2072 GGAGCTCTGCCACCGAGGGCGGCTCTGAGCTTACCAAGGTCTCTGTGCGTGTCCGCTCGCCAGCCCTGGGCGTGCAGCTACAGTGGGCTGGATGGGCA
691 W S S A T E A V P D V Y Q V S V P R L P A L G L G V L Q L Q L G L D G H
2181 CCGCAGCTCGCCCTCTCTGTGCGCATCTACTCGACGCGCGGAGCTGTGCGTCAGCAGGCAAGCGGTTCTCTCCGTGTGATCTGACTCTGGCACCAGCGACTTC
727 R T L P S S V R I Y L H G R Q L S V R H E A F L R V I D S G T S D F
2290 GCGCTCAGCAACCGCTACATGCAAGGTCTGGTTCTCAGGCGCTTACTGGGCTCTCAAGAGCATCCGAAGGGTGGATGAGGAGACAGCAGCAGGAGCTGGACATGCAAGTCC
764 A L S N R Y M Q V W F S G L T G L L K S I R R V D E E H E Q Q V D M Q V
2399 TTGTCTATGGCACCCGTACGTCCAAAGACAAGATGGAGCCTACCTCTTCTGCGCCGATGGCGAGGCTAGCCCTACGTCCCCAAGGAGCCCGGCTGTGGTGTCACT
800 L V Y G T R T S K D K S G A Y L F L P D G E A S T P S P R S P P C G V T
2508 GAAGGCCCTTCTTCTCAGAGGTGGTGGCTACTATGAGCAGATCACCAGCGGCTCGCGCTTACAATCTGCCAGGGGTGGAGGGGCTGTCTGGACATATCATCCC
836 K A L S S O R W L R T M S T F T R R S G F T I C O G W R G C L W T Y H P
2617 TGGTGGACATCCGGGACTACGTCAACAAGAGACTGGCCCTGCACATCCATACAGACATCGACAGCCAGGTTGACAGCCCGACGGTATCTGAAGAAGCTCCCCCTCAAG
873 W W T S G T T S T R S W P C T S I O T S T A R V Q P R R Y L K K L P L Q
2726 CCAACTCTACCCCTGCCAGTCTAGGCTATATCCAGGACGACAGAGCGCTCAGGCTGCACACTGCCAGGCGCTGGGTGTCTAGCCTCAAAGATGGCAGCT
909 A N F Y P M P V M A Y I Q D A Q K R L T L H T A Q A L G V S S L K D G Q L
2835 GGAGGTGATCTGGACCGCGGCTGATCGAGGATGACAAACCGGGCGCTAGGCGAAGGGCTCAAGGACAACAGAGAACTGCAACCGCTTCCGCGCTCTGCTAGAGCGG
945 E V I L D R R L M Q D D N R G L G O G L K D N K R T C N R F R L L E R
2944 CGAACCCTGGGCGAGTGAGTCCAAGATAGCCACTTACCAGCTACCCATCCCTCTCAGCAGCACTGACCTCCATGACTCTGAACGCGCCCGGCGCTCGCTCTGCTCTAG
982 R T V G S E V Q D S H S T S Y P S L L S H L T S M Y L N A P A L A L P V
3053 CAGGATGAGCTCCAGGCGCTGGTCTGGCTCATTTATCTCTGGCTTCTCACTGCGCTGTGACTTCCACCTGCTCAACCTACGTACGCTCCAGGCTGAGGAGGA
1018 A R M Q L P G P G L R S F M P L A T S S L P C D F H L L N R L L Q A E E D
3162 CACCCTACCTCTCGGCGGAGACCGCACTCATCTTACACCGCAAGGGTTTGTCTCGGCGCTGGAGGCGCAAGAATTTGGGCTTCAACTGCACCACAAGCCAAAGCAAGTA
1054 T L P S A E T T G A T G K G F D C G L E A K N L G F N C T T S Q G K V
3271 GCGCTGGGCGAGCTTTCCATGGCTGGATGTGGTATTCTTCAGCCAACTCTTGACGTTACTGTACCTCTGGCGCTCCCCGCTCCAACAGCAGTACGCTCTATTGG
1091 A L G S L F H G L D V V F L O P T S L T L Y P L A S P S N S T D V Y L
3380 AGGCCATGGAGATTGCTACCTTTCGCGCTCCGCTGGGTAG
1127 E P M E I A T F R L R L G

Insect cell mannosidase III (AF005034)

1 ATCAGGACTCGTGTCTCTCGTGTGCGGCGCTTCTCCACCCGGATCTGCTGCTGCTGCTATTTGTCTTGGGTTTGGGGCTCTACTGCTATTTTCAAAATGCATCTCTCA
111 M R T R V L R C R P F S T R I L L L L F V L A F G V Y C Y F Y N A S P Q
111 GAACATAACAAACCAAGATCAGTTACCCAGCAGTATGGAGCACTCAAAATCTTCCCTCACTACACCGTCAAGAGCGGACAGCCAACTCCGGATCAATGCCCTG
377 N Y N K P R I S Y P A S M E H F K S S L T H T V K S R D E P T P D Q C P
221 CATTGAAGGAAGCGAAGCGGACATCGACCGTGGCAGATATACCCAACTTTGATTTTACCGCAGTGGTGGCGTCAAAAGAAATTTGGGCAAGTCTTGGGAGGAT
747 A L K E S E A D I D T V A I Y P T F D F Q P S W L R T K E F W D K S F E D
331 CGGTATGAAGAATTCATACAGCACATACACCGCCTAGACTGAAGGTAAATCGTGTTCTCATCTACACAAACGACCGGATGGCTGAAGACGTTTGAACCACTACTTGA
111 R Y E R I H N D T T R P R L K V I V V P H S H N D P G W L K T F E Q Y F E
441 GTGGAAGACCAAGAACATTATCAACACATAGTGAACAACTGCACCGACCCCAACCACTGACCTTCATTTGGACCGAGATATCGTTTCTGAATCGCCTGGTGGGAAAGGT
1477 W K T K N I I N N I V N K L H Q Y P N M T F I W T E I S F L N A W E R
551 CGCAGCCTGTCAAAACAAAGGCTTGAAXAACTTATCAAGAAGGTCTGCTCGAGATCACGACGGGCGGCTGGGTGATGCCGACGAAGCTTGCAGCATATCTATGCG
184 S H P V K Q K A L K L K I E G R L E I T T G W V M P D E A C T H I Y A
661 CTAATTCACCAAGTTTATGAAGCACTCTGGGTGAAXAACTATCTCCGGCTCATCCGGAACAGGATGGTCTATTCACCCCTTCCGACCGGGGCACTGTGCCTTA
221 L I D Q F I E G H H W V K T N L G V I P K T G W S I D P F G H G A T V P Y
771 CCTGTAGACGAGCGCCTTGAGGGAACATTATACAGAGAATCCATTATCGGTGGAAXAAGTGGGTGGCGAGGACAGATGAGGAGTTTACTCGCTGGGAGGT
2577 L L D Q S G L E G T I I Q R I H Y A W K O W L A E R O C I E E F Y W L A S
881 GGGCTACTACGAAGCCCTCCATGATAGTGCACAACTCAGCCGTTTGATATTTCAATAAAGACAGCTGTGGCGCCGACCTTCAATTTGTCTCAGTTTCCACTTCAGG
294 W A T T K P S M I V H N Q P F D I Y S I K A S T G C G P H P S I C L S F D F R
991 AAGATTCCCGGCGAATTTCTGAATACACAGTAAAGCAGGAAGCATCGGGAACCAACTTGCACGACGAAGGCAAGAGCTTGTATAGAGGAGTACGACCGTATCGGGCT
331 K I P G E Y S E Y T A K H E D I T E H N L H S K A K T L I E E Y D R I G S
1101 CCTGACTCCACACAACGTTGGTCTGGTGGCGCTCGGAGCAGACTTCAGATACGAGTACAGGCTCGAGTTTGTATGCCCAATACGTCATTAATGAAATTTTAACTACA
367 L T P H N V L V L P L G D D F R Y E Y S V E F D A Q Y V N Y M K M F N Y
1211 TCAATGCTCAAGGAATTTCAACGCTGAGTCAGTTCGGAACCTCTCTCGATTACTTTAACCCTATGAAGAAGACATCAAAATATACCCAGCTTAAAGGGAGAT
404 I N A H K E I F N A D V O F G T P L D Y F N A M K R E H Q N I P S L K D
1321 TCTTCTGTTTACGATATTTTACGGAAGGTAAACAGGCTACTGGTCAGGTTACTACTACTACCACTTACCAAAATTTCTCCGGCTCAGTTTGCACCAACCAACT
443 F V V Y S D I F S E G K P A Y W S G Y Y T T R P Y Q K I L A R Q F E H Q L
1431 CGGATCGGCGAGATTTTATCACCCTTGTATCGAACTACATCAGACAGATGGGTCCGCAAGGAGAGCTTCGGAGCTTCTGAGAAAAGTTAGAAAATTTTACGAGC
477 R S A E I L F T L V S N I R O M G R Q G E F G A S E K K L E K S V E Q
1541 TTATCTATGCTCGACGGAATTTGGGTCTGTTTCAACATCAGATCGGATTTACTGGAACATCAAGTCCAGTGTGATGCAAGATTTACGGAACCAAACTTTCACAAGTCTG
514 L I Y A R R N L G L F O H H D A I T G T S K S S V M O D Y G T K L T F T L
1651 TATCATGCTATCGGCTCGAGGAGGCGCGCTCACCACCATCATGTTGGCTGACCACTGTTGCACTCGCAGGAGCATATACAAAGCGAGGTTGAGTGGGAATCTACGG
551 Y H C I R L O E A L T T I M L P D Q S L H S Q S I I Q S E V E W E T Y G
1761 AAAACCGCCCAAGAGCTGCAAGTGTCTTTCATTGACAAGAAGAAAGTTTAACTTTTAAATCCGTTGGCTGAGACTCGAACTGAAGTGGTCACGGTTAGATCCAACAGT
587 K P P K K L Q V S F I D K K V I L F N P L A E T R T E V T V R S N
1871 CCAACATCCGGGTGATACATACACAAGAGGAGGACAGCTCTGTATCAGATAATGCCACGACATCAATCCAAGACAAAGCGGAAGAGATCGTAAGCGACACACCGTTC
624 S N I R V Y D T H K R K H V L Y Q I M P S I A T I O D N G K S I V S O T F
1981 CACATAATGTTCTGGGCGACATTCGCGCCCTCACCCTCATCTGTAACAAGTGCAGGAGCACCACCACTTCCACCACTCGGTCATTTTTCGCAACCACTGCGAACA
661 D I M F V A T L H P T L S I S Y K L O E H T T S H H C V I F C N N C E Q
2091 ATACAGAGAATCCAATGTCTTCCAAATTAAGAAAATGATGCTGGTGACATCAAAATAGAAAATGCAGTGCTAAAACTTCTCGTTAATAGGAACACCGGCTTCTGAGAC
697 Y O K S N V F O I K K M M P G O I O L E N A V L K L L V N R N T G F L R
2201 AAGTCTATGAAGAAGACATCCGGAAGGAGAACTGCTGTTGAGCTCAAAATTCGGCGCATATCAAGTCCGCAAGACATTTCTGGTGTCTACTCTTCTATCGCTTACTACGAC
734 Q V Y R K D I R K T R V D V O F G A Y O S A Q R H S G A Y L F M P H Y D
2311 TCACCTGAGAAGAATGTTCTGCATCCTACACTAATCAGAACCAACTGCAAGATGATAACATATCATAGTCTCGGACACTATTTTACGGAATACAGGACCTGTACTT
771 S P E K N V L H P Y T N O N N M Q D D N I I V S G P I S T E I T T M Y L
2422 CCGCTTCTTGGTGACACTATTAGGATATAACAAGTGGCGGACCGGATCTGTCGGGTGCTATTTCTATTAGAGACCGATGATGATTTTCGAGGCGCCACCTAAGAACAGAG
807 P F L V T H T I R I Y N V P D P V L S R A I L L E T D V D F E A P P K N R
2511 AGACTGAGGTTATTATGAGATTACAGACTATATCAAAACGGTGACATTCGGAATTTTACCCGATCAGAACCGATTCCAGTACCAAAAGAGGGTCAAGTGAATATAA
844 E T E L A F M R L Q T D I P E F Y T D O N G F Q Y O K R V K V N K
2641 CTAGGAATAGAAGTAACTATACCAGTACTACCTACCATGGCGTCCCTGCAAGACGAGGAGACCGGCTCAGTCTGTCAGCAACACCGCTCAAGCGGCTGCTGATACGA
881 L G I E A N Y P I T T M A C L Q D E E T R L T L T N H A Q G A A Y E
2751 ACCGAGACGCTTAAAGACTCATGCTCGATCGTCCAACCTTTATGATGACTTCAGAGGAAATCGGTGAAGGAGTATGCTGATAACAAACCGGACCTTCCAGAACTGGATTT
917 P G R L E V M L D R R T L Y D D F R G I E G V V D N K P T T F O N W I
2861 TAAITGAATCCATGCCAGGCGTGAAGGCGCAAGAGAGACACTAGTGAACACAGTTTCAAAATTTGTTAATGAAGCTGGTTTGGCCCGGGCGCAAGGAAAGCCCTTAC
954 L I E S M P G V T R A K R D T S E P G F K V N E R R F G P G Q K E S P Y
2971 CAAGTACCGTCCGAGACTGCGGACTACCTGAGCAGGATGTTCAATTACCCGGTGAACGCTGACTCTGGTGGACACTAGCGAGGTTGGCGAGATCGAGGTGAAGCGGTACCA
991 Q V P S Q T A D Y L S R M F N Y P V N V Y L V D T S E V G E I E V K P Y Q
3081 GTGCTTCTCGAGAGCTTCCCGCCCGGACTCACCCTGGTCACTTCCGCACTCACGACGAGTGTGCAACTTCTCCCAAGCAAGAGCTACATGGTACTGCAC
1027 S F L Q S F P P G I H L V T L R T I T D D V L E L F P S N E S Y M V L H
3191 GACCAGGATACAGTCCGCTGTGGAGAGAAGCCAGTCCCAAGTCTCCCAAGTTTTCGTCAAAACAGGTTCAATGGTCTGAACATTCAGAACATCAGTCACTGAGTCA
1064 R P G Y S C A V G E K P V A S P K F S S K T R F N G L N I O N I T A V S
3301 CTGACGGGCTGAAGTCACTCCGACCTCTCAGAGTCTGAGTGACATCCACTGAACGCTATCGAGGTAAAAACTTCAAGATCAGGTTTAA
1101 L T G L K S L R P L T G L S D I L N A M E V K T Y K I R F

FIG. 34

Human lysosomal mannosidase II (NM_000528)

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1  ATGGGCTACGCGCGGGCTTCGGGGGCTCGCGCTCGCGGCTGCTGGACTCAGCAGGCCCTGGACCATGTCCCGGCGCTCGCGCCACCGCTCCCGCTCTCTGCTTTT
10  M G Y A R A S G V C A R G C L D S A G P W T M S R A L R P P L P P L C F
110 TCCTTTTGTGCTGGCGGCTGCGGCTGCTCGGGCGGGGATACGAGACATGCCCCACAGTGCAGCCGAACATGCTGAACGTGCACCTGCTGCTCAGACACATGATGA
37  F L L L L A A A G A R A G G Y E T C P T V Q P N M L N V H L L P H T H D D
219 CGTGGGCTGGCTCAAAACCGTGGACCACTACTTTATGGAATCAAGAAATGACATCCAGCAGCGCGGTGTGCAGTACATCTGGACTCGGTCACTCTGCTGCTGCTGGCA
73  V G W L K T V D Q Y F Y G I K N D I Q H A G V Q Y I L D S V I S A L L A
328 GATCCACCCCGTTCCTTACCTGGAGATTGCTTCTTCTCCGCTTGGTGGCCAGCAGCAGCAAAATGCCACACAGGAAGTCTGCGGAGACCTTGTGCGCCAGGGGC
110  D P T R R F I Y V E I A F F S R W W H Q O T N A T Q E V V R D L V R Q G
437 GCCTGGAGTTTCCCAATGGTGGCTGGGTGATGAACGATGAGGCAGCCACCCACTACGGTGGCATCGTGGACAGATGACACTTGGGCTGCGCTTCTGGAGGACACATT
146  R L E F A N G G W V M N D E A A T H Y G A I V D Q M T L G L R F L E D T F
546 TGGCAATGATGGCGGACCCCGTGTGGCTGGCACATTGACCCCTTCGGCCACTCTCGGGAGCAGGGCTCGCTGTTTGGCGAGATGGGCTTCGACGGCTTCTTCTTGGG
182  G N D G R P R V A W H I D P F G H S R E Q A S L F A Q M G F D G F F F G
655 CGCCTTGATTATCAAGATAAGTGGGTACGGATGCGAAGCTGGAGATGGAGCAGGTGTGGCGGGCCAGCAGCAGCTGAAGCCCCGACCGCGGACCTTCTCACTGGTG
219  R L D Y Q D K W V R M Q K L E M E Q V W R A S T S L K P P T A D L F T G
764 TGCTTCCCAATGGTTACAAACCCGCAAGGAATCTGTGCTGGCATGTGCTGTGTCGATCAGCCGCTGGTGGAGGACCTTCGAGCCCGGAGTACAAACGCAAGGAGCT
255  V L P N G Y N P P R N L C W D V L C V D Q P L V E D P R S P E Y N A K E L
873 GGTGATTAATCTCTAAATGTGGCCACTGCCAGGGCCGCTATTACCGCACCAACACACTGTGATGACCATGGGCTCGGACTTCCAATATGAGAATGCCAACATGTGG
291  V D Y F L N V A T A Q G R Y Y R T N H T V M T M G S D F Q Y E N A N M W
982 TTCAAGAACCTTGACAAAGCTCATCGGCTGGTAAATGCCGAGCGGCAAGGAAAGGACAGTGTCCATGTTCTCTACTCCACCCCGCTTGTACTCTGGGAGCTGAACA
328  F K N L D K L I R L V N A Q Q A K G S S V H V L Y S T P A C Y L W E L N
1091 AGGCCAATCTCACTGGTCACTGAAACATGACCACTTCTTCCCTTACGCGGATGGCCCCCAGCTTCTGGACCGGTTACTTTTCCAGTCCGCGCGGCTTCAAAACGCTA
364  K A N L T W S V K H D D F F P Y A D G P H Q F W T G G Y F S S R P A L K R Y
1200 CGAGCGCCTCAGCTACAATCTCTGAGGTGTGCAACCACTGGAGCGCTGGTGGCGCTGGCGGCAACCTGGGACCTTGGCTCGGAGACAGTGCACCCCTCAAT
400  E R L S Y N F L Q V C N O L E A L V G L A A N V G P Y G S O D S A P L N
1309 GAGGCGCTGGCTGTGCTCAGCATCAGCAGCGCTCAGCGGCACTCCCGCAGCAGCTGGCCAAAGCTAGCGCGCCAGCTTGGCGGAGCTTGGGGGCTTGGCAGG
437  E A M A V L Q H H D A V S G T S R Q H V A N D Y A R Q L A A G W G P C E
1418 TTCTTCTGAGCAACGCGCTGGCGCGGCTCAGAGGCTTCAAGATCACTTCACTTTTCCCAACAGCTAAACATCAGCATCTGCCCGCTCAGCCAGCAGCGCGCGCTT
473  V L L S N A L A R L R G F K D H F T G C Q Q L N I S I C P L S Q T A R F
1527 CCAGGTCACTGTTTATAATCCCTTGGGCGGAAGGTGAATGGATGGTACGGCTGCCCGTCAAGCAAGGCGTTTTCGTTGTGAAGGACCCCAATGGCAGGACAGTGCCT
509  Q V I V Y N P L G R K V N W M V R L P V S E G V F V V K D P N Q R T V P
1636 AGCGATGTGGTAAATATTTCCAGCTCAGCAGCGCAGCGGCACTTCCGAGCTGCTGTTCTCAGCTCACTGCCCGCTTGGGCTTCAAGCACTATTCACTAGGCCAGG
546  S D V V I F P S S D S Q A H P P E L L F S A S L P A L G F S T Y S V A Q
1745 TGCTTGGTGGAGCGCCGCGGCGGCGCAGCCAGCCATCCCCAGAAAGATCTGGTCCCCGCTTAAACCATCGAAATGAGCAGATCCGGGCAACGTTTGTATCTGA
582  V P R W K P Q A R A P Q P I P R R S W S P A L T I E N E M I R A T F D P D
1854 CACAGGGCTGTTGATGGAGATTATGAACATGAATCAGCAACTCTGCTGCTGTTCCGCGAGACCTTCTTCTGTTACAACCCAGTATAGGTGACAACGAAAGTGAACAG
618  T G L M E I M N M N O Q L L L P V R O T F F W Y N A S I G D N E S D Q
1963 GCCTCAGGTGCTTACATCTTCAAGCCCAACCAAGAAACCGCTGCTGAGCGCGCTGGGCTCAGATCCACTGGTGAAGACACCCCTTGGTGCAGGAGGTGCACACAGA
655  A S G A Y I F R P N Q O K P L P V S R W A Q I H L V K T P L V Q E V H Q
2072 ACTTCTCAGCTTGGTGTTCAGGTTGGTTCGCTGTACCCAGGACAGCGGCACTGGAGCTAGAGTGGTGGTGGGCGGATACCTGTGGCGGACACCTGGGGGAAGGA
691  N F S A W C S Q V V R L Y P G O R H L E L E W S V G P I P V G D T W G K E
2181 GGTCACTCAGCCCTTTTGACACACCGCTGGAGACAAAGGACGCTTCTACACAGCAGCAATGGCCGGGAGATCTGGAGAGGAGGCGGGATTATCGACCCACTCGAAA
727  V I S R F D T P L E T K G R F Y T D S N G R E I L E R R R D Y R P T W K
2290 CTGAACACAGCGGAGCCGCTGGCAGGAACTACTATCCAGTCAACACCCGATTTACATCAGGATGGAAACATGCAGCTGACTGTGCTGACTGACCGCTCCGAGGGG
764  L N Q T E P V A G N Y Y P V N T R I Y I T D G N M O L T V L T D R S O G
2399 GCAGCAGCTCAGAGATGGCTGCTGGAGCTCATGGTGCACCGAAGGCTGCTGAAGGACGATGCAGCGCGGATATCCGAGCCACTAATGGAGAACCGGTCCGGGGCGTG
800  G S S L R D G S L E L M V H R R L L K D D G R G V S E P L M E N G S G A W
2508 GGTCCGAGGGCGCCACTGGTGTGCTGGACACAGCCAGGCTGCAGCCCGGACACCGGCTCTGGCGGAGCAGGAGGTCTGGGCCCCCTCAGGTGGTGGTGGCCCCG
836  V R G R H L V L L D T A Q A A A G H R L L A E Q E V L A P Q V V L A P
2617 GGTGGCGGCGCGCTACAATCTCGGGGCTCTCCGCGCAGCGAGTCTCAGGGCTCGCGAGGAGCTGCCGCTTCCGTGCACCTGCTCAGCTGGCCAGCTGGGGCC
873  G G G A A Y N L G A P P R T O F S Q L R R D L P P S V H L L T L A S W G
2726 CCGAAATGGTGTGCTGCGCTTGGAGCAGCAGTTTCCGCTAGGAGAGGATTCCGGACGTAACCTCAGCGCCCCGTTACCTTGAACCTCAGGAGCTGTTCTCACCTT
909  P E M V L L R L E H Q F A V G E D S G R N L S A P V T L N L R D L F S T F
2835 CACCATCACCCGCTGCAGGAGACACAGCTGGTGGCCAAACAGTCCCGAGGCGAGCTCCAGGCTCAAGTGGACAAACAAACAGGCCCCACACCCCAACCAACTCCG
945  T I T R L Q E T T L V A N O L R E A A S R L K W T T N T G P T P H Q T P
2944 TACCAGCTGGACCGGCGCAACATCAGCTGGAACCCATGGAATCCGCACTTCTCGGCTCAGTTCAATGGAAGGAGTGGATGGTTAG
982  Y Q L D P A N I T L E P M E I R T F L A S V Q W K E V D G

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FIG. 35

Human cytoplasmic mannosidase II (NM_006715)

1 ATGGCGGCGAGCCGCGTTCTTGAAGCACTGGCGACCACCTTTTGAAGGGGTGGAGAAGTTCGTGTCCCGGATCTACTTCAACCACTGTAACCTCCGCGGCGAGGCTTTTGG
1 MAAACAGPFLKHWRITTFERVEKFVSPGYFTDCNLRGLF
110 GGGCAGCTGCCCTGTGGCTGTCTCCAGCTTCTGACGCGGAGAGACTTCCCTACGAGGAGGACTCAGCGGGCACTTCCGCGCGGCGAGCTCGGCGCAGCTT
37 G A S C P V A V L S S F L T P E R L P Y Q E A V O R D F R P A Q V G D S F
219 CGGACCCACATGGTGGACCTGCTGGTTCGGGTGGAGCTGACCATTCCAGAGGCACTGGGTGGGCGCAGGAAGTTCACCTTGTGGGAAAGTGAQVAGAGGCTCGGTG
71 G P T W T W T C W F R V E L T I P E A W V G Q E V H L C W E S D G E G L V
328 TGGCGTGATGGAGAAGCTGTCCAGGTTTAAACAAAGAGGGGTGAGAAGCAAGCTATGCTCTGACTGACAGGCTGGGGGAAAGCAACCCCGAAGGCTCCTCTCTATG
110 W R D G E P V O G L T K E G E K T S Y V L T D R L G E R D P R S L T L Y
437 TGGAAAGTAGCCTGCAATGGGCTCTGGGGGCGGGGAAGGGAAGCATGATTGACGCCCTGACCTGAGAAGATATTCAAGTGAGCGGGCTGAGCTAGCTGTGTGTCA
146 V E V A C A N G L L G A G K G S M I A A P D P E K I F Q L S R A E L A V F H
546 CGGGATGTCACATGCTCTGTGGTGTGAGGCTGCTGGGCAATAGCCAAGGCGCTGGGGAAGGCAACACAGCGAGCTTCCAGGCGCTGTACACAGCCAACTCAG
182 R D V H M L L V D L E L L L G I A K G L G K D N Q R S F Q A L Y T A N Q
655 ATGGTGAACGCTGTGACCTGCCAGCCGAGACCTTCCAGTGGCCAGGCTGGCTCAGGTTTCTGGCCAATGGGGGTGAAAGGCAACACACCACTTCATG
219 M V N V C D P A Q P E T F V A Q A L A S R F F G O H G G E S O H T I H
764 CACAGGAGCTGCCACATGATACAGCTGGCTTTGGCCCTTCAAAGAGACTGTGAGGAAATGTGCCCGAGCTGGGTCAACCGCTGAGCTCATGGAGCGGAACCC
255 A T G H C H I D T A W L W P F K E T V R K C A R S W V T A L Q L M E R N P
873 TGAGTTCATCTTGGCTGCTCCAGGCGCAGCAGCTGGAATGGGTGAAGAGCGCGTACCTGGCTGTACTCCCGCATCCAGGAGTTCGGTGGCGTGGGCACTTTGTG
291 E F I F A C S Q A Q L E W V K S R Y P G L Y S R I Q E F A C R G Q F V
982 C T G T G G G G G C A C T G G G T G G A A T G G A T G G G A A C T G C C A G T G G A G G C C A T G G T G A G G C A G T T T G C A G G G C A G A A C T C T T T C T C A G G A G T T T G G G A A G A
328 P V G G T G W E M D G N L P S G E A M V R Q F L L G O N F F L Q E F G K
1091 TGGTCTTGAGTTTGGCTGCGGCAAGCTTTGGCTACTCAGCAGCACTCCCCAGATCATGCAGGCTGTGGCATCAGGCGCTTTCTCACCAGAAATGAGCTGGAA
364 M C S E F W L P D T F G Y S A Q L P Q I M H G C G I R R F L T O K L S W N
1200 TTTGGTGAACCTCTTCCCAACCACTATCTTTTGGAGGGCTGGATGGCTCCGCTGACTGGTCACTTCCCACTGGGCACTCTATGGGATGAGGGCAGCGTG
400 L V N S F P H F W E G L D G S R V L V H F P P G D S G M Q G S V
1309 CAGGAGGTGCTGAAGACCGTGGCCAAACACCGGCAAGGGGCGGCGCAACCAAGTGCCTTCTCTTGGGTTTGGGATGGGGGTGGTGGCCCAACCAAGCACTGC
437 E E V L K T V A N N R D K G R A N H S A F L F G F G D G G G O P T Q T M
1418 TGGACCGCTGAAGCGCTCAGCAATACGGAATGGGTGGCCAGGTCGAGCTATCTTCCAAGACAGCTCTTCTCAGCAGCTGGAGAGTGCATCAGAGCAGCTGTGCAC
473 L D R L K R L S N T D G L P R V O L S S P R Q L F S A L E S D S E Q L C T
1527 CTGGGTTGGGAGCTCTTCTGGAGCTGCACAATGGCAATACACCAACCTGCCAGATCAAGAAGGGGCAACCGGGAATGTGAGCGGATCTGCACAGCAGCTGGAGCTG
509 W V G L E L H N G T Y T H A Q I K K G N R E C E R I L H O V E L
1636 CTGACTAGCCTGGCCCTGGCCCGCAGTGGCCAGTTCCTATACCCAGCAGCCAGCTGCAGCAGCTCTGGAGGCTCTTCTTCTGAACAGTTCATGATGTGGTGAAGT
546 L S S L A L A R S A O F L Y P A A Q L H L W R L L L N Q F H D V T
1745 GAAGTGCATCAGATGGTGGCAGGAGAAGCATGTGCCATTATGAAGACATCCGTTCCATGGCAATACACTGCTCAGCGCTGCAGCGCAGCGCTGTGTGCTGGGA
582 G S C I Q M V A E A M C H Y E D I R S H G N T L L S A A A A L C A G E
1854 GCCAGGTCCTGAGGCGCTCTCATGTCAACACACTGCCCTGGAAGCGGATGAAGTGAATGGCCCTGCCAAACCGGGCGGGCCAGCAGCTAGCCCTGGTCAAGT
618 P G P E G L L I V N T L P W K R I E V M A L P K P G G A G S L A L V T V
1963 CCGCAGCTGGGCTATGCTCTGTTCTTCCCCACCTCACTGCAGCGCTGTGCCCGCAGCAGCTGTGTCGTAGTGAAGAGACTGATGGCTCGTCACTTGCGA
655 P S M G Y A P V P P P T S L Q P L L P Q Q P V F V V Q E T D G S V T L D
2072 ATGGCACTCCAGTGAAGCTGGACCACTGTGCGCTGAGCTCTTGGTCTGTGGTGGCTTGGCAGGAGGCAATGCTCAGGGCGCGCTGGGGAACCACTTTGT
691 N G I I R V K L D C T T G R L T S L V L V A S G R E A I E A G A V N Q F V
2181 GCTATTGATGATGCTCCCTTGTACTGGGATGCATGGGAGCTCATGCACTACCACTGGAGACAAGGAGCTGTGCTGGGCGAGGCAAGCACTGGCAGTGGGACC
727 L F D V P L Y W D A W D V M D Y H L E T R K P V L G O A G T L A V G T
2290 GAGGCGCGGCTGGGGGCGAGCGCTGGTCTTGTCTACAGATAGCGCCCAACAGTGGGCTTAGCCAGGAGGTTGTGCTGGACGTTGGCTGCCCTATGTCCGCTCCACA
764 E G G L R G S A W F L L O I S P N S R L S Q E V L D V G C P V R F H
2399 CCGAGGTACCTGGCATGAGGCGCAAGTTCCTGAAGGTGGAGTTCCTGCTCGGCTGGGAGTTCAGGCGCACTATGAGATCCAGTTTGGGCACTTGCAGCGACC
800 T E V H W H E A H K F L K V E F P A R V R S S O A T Y E I Q F G H L Q R P
2508 TACCACTACAATACCTTTGGAGCTGGGCTGATTGTAGGTTGGGCGCATCGCTGGATGATCTGTGAGAACACCGGCTTGGGCTGGCCCTGCTCAAGCACTGCAAG
836 T H Y N T S W D W A R F E V W A H R W M D L S E H G F G L A L L N D C K
2617 TATGGCGCTCAGTGCAGGCGCAGCATCTCAGCTCTCGCTCTTGGGGCGGCTTAAAGCCCGGAGCAGTACTGCTGACACGGGCGGCGCCAGGCTCAGCTATGCAGCTGA
873 Y G A S V R G S I L S L S L L R A P K A P D A T A D T G R H E F Y A L
2726 TGCCCGCAAGGGCTCTTTCAGGATGCTGGCGGTTTCAAGTGCCTACAGCTTAACTTCCCCCTGTGGCTTGCAGCGCCCCAGCCAGCCCCCGCCAGCTCTGT
509 M P H K G S F O D A G V I O A Y S L N F L L A L P A S P A P A T S W
2835 GAGTGGCTTTTCGTGTCTTACCCTGGGCTCGATTGGAGACCGTCAAGCAGGCGGAGAGCAGCCCCAGCGCGGCTCGTGGTCTGAGGCTGTATGAGGCGAGCGGC
945 S A F S V S S P A V L E T V K Q A E S P O R S L V L R L Y E A H G
2944 AGCCACGTGAGCTGGTGGCTGCACTTGCCTCGCGGTTGAGGAGGAGCACTCTCGCATCTCTGGAGCGACAGACCTTGTGGCCACTTGACTTGGGACAACCGC
982 S H V D C W L H L V P V Q E A I L C D L L E R P D P A G H L T S G Q P
3053 CTGAAGCTCAGCTTCTTCTTCCAAAGTGTGTCCGTGTGCTGTGCTCAGCTCCGCGACACTGAGTCCCTGGGGCTGGGGTTTGTGTGAAGGCTCTGGG
1018 P E A H L F S L P S A V P V A R A S A S A T L S P W G W G F V C R R L C T G G G
3162 ACTCTCAATTTCTGCTTCCCCAGCTAA
1054 L L I S A S P A

Figure 36A

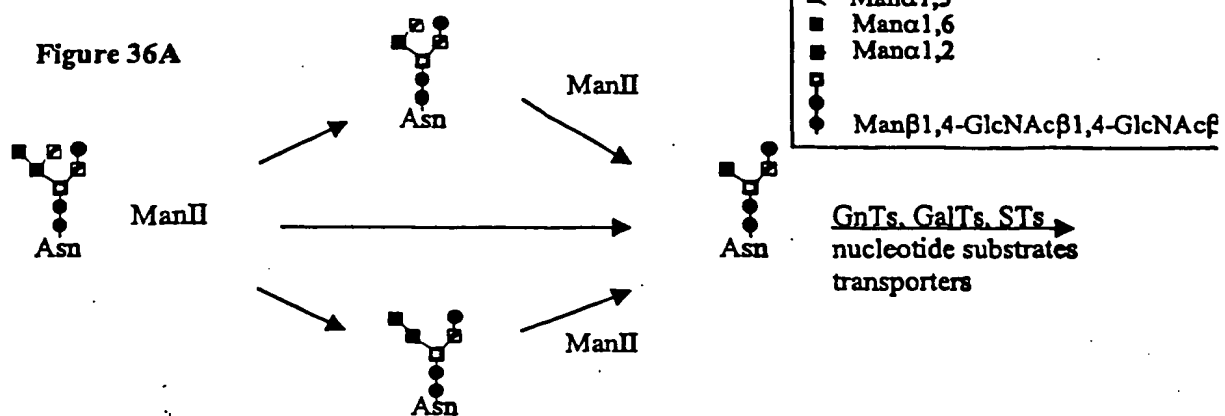


Figure 36B

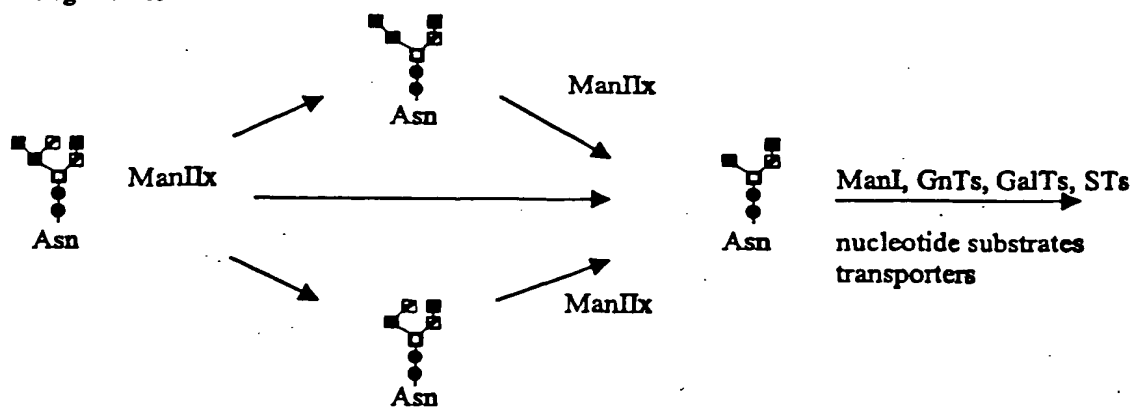


Figure 36C

